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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred
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2: /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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3: /SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390729 seqs, 57163235 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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113	122	123.5	126	126.5	144	155	155	195.5	1061	1061	Score	
10.7	11.5	11.6	11.9	11.9	13.6	14.6	14.6	18.4	100.0	100.0	Query Match Length DB	ф
211										205	ength [
21	2	21	21	21	21	20	17	21	21	21	:	
B01789	Y99598	В11637	B01788	B01786	B40407	W73358	R87527	B01787	Y79298	Y99597	ID	SOMMANTES
Escherichia coli Y	E coli Ithreonin	A. vitis hypersens	Escherichia coli Y	Escherichia coli Y	Human ORFX ORF171	S. colwelliana Mlq	Mel-linked mlqA qe	Escherichia coli Y	E. coli RhtB prote	E. coli L-homoseri	Description	

Novel Escherichia bacterium having enhanced L-threonine resistance to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -

due

Amino acid sequenc	Y34877	20	468	•	72	45
GPR2 prote	B01449	21	362	6.9	73	44
lulose	W60039	19	974	•	(4)	43
	W73308	19	974	•	(4)	42
Eucalyptus grandis	в16338	21	955		73.5	41
nneı	W20731	18	375			40
murium po	W80604	19	153		1.1	39
ndida albicans	Y96164	21	783		74	38
5	Y01649	20	551		74	37
meningi	Y38698	20	277		74	36
dia p	Y35106	20	465	•	4	35
cid sequen	Y29197	20	170		4	34
Murine Int6 protei	W02113	17	396		1 D	33
Human homoloque of	W02112	17	396		75.5	32
Neisseria meningit	Y38699	20	277		40	31
Mouse OCTN1 amino	в20579	21	553		76	30
A protein with cat	Y01651	20	553		76	29
Arabidopsis thalia	G12757	21	276		\sim	28
ŝ	G12758	21	272		\sim	27
	G51075	21	246		•	26
İS	G12759	21	243		76.5	25
ÇO.	G51076	21	242		~	24
Arabidopsis thalia	G51077	21	213		~	23
	W20694	18	539		77	22
	W20330	18	496		77	21
seria	Y38789	20	513		~	20
eisseria q	Y38788	20	513		78.5	19
	Y09517	20	615		79	18
. elegans	Y09518	20	596		79	17
	Y38702	20	307		79.5	16
onorrh	Y38701	20	307		79.5	15
Η:	Y04105	20	517		80	14
rthrobacter nico	Y04104	20	484		80	13
C. qlutamicum Lys	W37715	18	236		89.5	12

ALIGNMENTS

RESULT Y99597 WPI; 2000-414602/36. N-PSDB; A48442. Livshits VA, 23-DEC-1998; 20-DEC-1999; 28-JUN-2000. EP1013765-A1 Escherichia coli. L-homoserine resistance; L-homoserine synthesis; rhtB; L-threonine; L-valine; L-leucine. E. coli L-homoserine resistance protein, RhtB 08-SEP-2000 (first entry) (AJIN) AJINOMOTO KK. Y99597; Y99597 standard; Zakataeva NP, 99EP-0125406 98RU-0123511 Protein; 205 Aleshin VV, Ā Belareva AV, Tokhmakova IL;

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В
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Y79298
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Best Local S
Matches 205
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                                                                                                                                                                                                                                                                                                                                                            18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                      Y79298;
                                                                                                                                                                                                                                                                                                                                                                                                              Y79298 standard; Protein; 205 AA.
                      Novel RhtB protein, useful for generation of L-homoserine resistance Escherichia bacteria and large-scale production of e.g. L-homoserine
                                                            WPI; 2000-273530/24.
N-PSDB; Z94405.
                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                            L-isoleucine; L-valine;
                                                                                                                                                                                                                                                                                                         Homoserine resistance; RhtB protein; L-homoserine; L-alanine;
                                                                                                 Livshits VA,
Tokhmakova IL;
                                                                                                                                      (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                               13-OCT-1998;
                                                                                                                                                                                          20-SEP-1999;
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            L-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKALNKIFGSLFMLVGALLASARHA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mkalnkifgslfmlvgallasarha 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 AA;
                                                                                                                                                                                                                                                                      coli.
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                                                                                                                                                                                                                                                                                                                                protein imparting homoserine resistance
                                                                                                               Zakataeva NP,
                                                                                                                                                               98RU-0118425
                                                                                                                                                                                          99EP-0118581
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                                                                                                               Aleoshin VV,
                                                                                                               Belareova
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RESULT BO1787
ID BO1787
XX BO
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Matches 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the novel Escherichia coli K-12 protein, RhtB, which participates in resistance to L-homoserine. Amplification of the rhtB gene (see Z94405) results in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli; yeaS gene; amino acid production; excretion protein gene;
amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B01787 standard; Protein;
                                                                                                                                                                   30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli YeaS amino acid excretion protein
                             Tokhmakova IL;
                                                                                                                                                                                                                                                          17-DEC-1999;
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                                                           Livshits VA,
                                                                                                              (AJIN ) AJINOMOTO CO
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                                                           Zakataeva NP,
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99RU-0104431.
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                                                           Nakanishi K,
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                                                              Aleshin VV,
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                                                              Troshin PV;
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Matches 61
                                                                                  08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the YeaS amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, valine, histidine, isolaucine, glutamic acid and proise achieved if multiple copies of its gene are transfected into a
                                                                                                                                                                                                                                        Marine melA; selectable marker; oyster larva settlement; pigmentation; melanin; p-hydroxyphenylpyruvate-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-414802/36.
N-PSDB; A52689.
WPI; 1996-039515/04.
N-PSDB; T06767.
                                                                                                                                                         12-DEC-1995
                                                                                                                                                                                 US5474933-A.
                                                                                                                                                                                                       Shewanella colwelliana
                                                                                                                                                                                                                                                                             Mel-linked mlgA gene product.
                                                                                                                                                                                                                                                                                                     01-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                               R87527
                                                                                                                                                                                                                                                                                                                                                    R87527 standard; Protein; 153
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                                                                                                                                  21-MAR-1990;
                                                           (UYMA-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RIALWIKGPKQM-KALNKIFGSLFMLVGALLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           awagvatlikttpilfnivrylgafyllylgskilyat----lkgknseaksdepgygai 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEWWFAYLLTSIILTLSPGSGAI----NTMTTSLNHGYPAG-GVYCWASDRTGDSYC--A 55
                                                                                                                                                                                                                                                                                                                                                                                                             fvtqyirtkkklakvgnsliglmfvgfaarlat 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                           fkralilsltnpkailfyvsffvqfidvnaphtgisffilaatlelvsfcylsfliisga 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK---SLASTQSRRH--L 110
                                   νς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The bacterium used is E. coli.
                                   Weiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                           MARYLAND BALTIMORE
                                                                                           93US-0148945.
90US-0496804.
                                                                                                                                 90US-0496804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29pp;
                                    RM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid exc
                                                                                                                                                                                                        strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 195.5; DB 21; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                               07-JUN-1995;
21-MAR-1990;
10-NOV-1992;
08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colvelliana melA gene (T06766), and was designated mlgA (mel-linked gene). The role of the encoded protein (R87527) was unclear as deletion subcloning in E. coli demonstrated that only melA was require
                                                                                                                                                                                                                                                                                                                        ß
                                       MelA melanin protein e.g. cosmetics
                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                             US5846531-A.
                                                                                                                                                                                                                                                                   Shewanella colwelliana
                                                                                                                                                                                                                                                                                       MlgA; marine bacterium; melanin synthesis; marine exopolysaccharide; UV blocker; sunscreen; MelA.
                                                                                                                                                                                                                                                                                                                                            11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                W73358;
                                                                                                                                                                                                                                                                                                                                                                                     W73358 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oyster settlement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing larval
                  Example 7; Fig 13; 57pp; English.
                                                                       N-PSDB; V08553
                                                                                  WPI; 1999-058995/05
                                                                                                                                                                                                                          08-DEC-1998
                                                                                                                          (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tor melanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        138 fsmlayas 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                         G
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVMIGYAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dntssqlsnralitggfvtalanpkgwafmisllppfisvdqalapqlmvllslimmtef 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AA;
                                                                                                       Weiner RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
                                                                                                                                               90US-0496804.
92US-0974837.
93US-0148945.
                                                                                                                                                                                                     95US-0476254.
                                                                                                                                                                                                                                                                                                                      MlgA protein sequence
                                                                                                                                                                                95US-0476254.
                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.68; 29.78;
                                                   from marine bacteria
                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 155; DB 17;
Pred. No. 6.6e-10;
1; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                      Ą
                                                   1
                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                   as
                                                   9
                                                   blocker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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This sequence is

the Shewanella colwelliana

MlgA protein,

which

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RESULT
B40407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
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Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; hope demand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF171 polypeptide sequence SEQ ID NO:342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B40407 standard; Protein; 130 AA.
                                                                                                                                                                                                                                                                                            Homo sapiens
N-PSDB;
                                                                                                                                             31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                             31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                              05-OCT-2000
                                                                                                                                                                                                                                                               WO200058473-A2
                                                                                                                                                                                                                                                                                                                             thrombosis; contraceptive.
                                                Shimkets
                                                                             (CURA-) CURAGEN CORP.
                                                                                                              30-MAR-2000;
                                                                                                                               05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 fsmlayas 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 IVMIGYAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dntssqisnralitqgfvtaianpkgwafmisllppfisvdqaiapqlmvllsiimmtef 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|wmmvgelagvalvaiaavmgvasmmlnypqlfdilkwvgglylgyigismwrakgkmanl|
               2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                              RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                             cartilage damage; antiinflammatory disease;
                                                                                                                2000US-0540763
                                                Leach M;
                                                                                                                              99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 155; DB 20;
Pred. No. 6.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 18;
                                                                                                                                                                                                                                                                                                                                                coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antihacterial; antifurgal; antifungal; antitheumatic; antithyroid; antihacemic. The antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRY-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune discorders are the severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C74446 to
   Sequence
                                                                                     disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent the human ORFX open reading frames 1 to 3161. The esquences have activities such as: cytostatic; hepatotropic;
                                                      enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C77606 encode the proteins given in B40237 to B43397, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 608; 5507pp; English.
   130
      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFX
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Matches
                                                                                                                                                                       Query Match
                                                              139 --QQPQLMQYIVLGVTTIVVDIIVMIGYATLAQ--RIALWIKGPKQMKALNKIFGSLFML 194
121 lglnlafaq 129
                       195 VGALLASAR 203
                                             63 ggtapal-qmlv1sgvfmamtlavfvlygllanvfrrav-vesprvqnwlrrsfatafag
                                                                                                                    79 AAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMP 138
                                                                                                                                                           Local
                                                                                               ω
                                                                                              1 Similarity 40; Conserv
                                                                                                                                              Conservative
                                                                                                                                                           13.6%;
31.0%;
                                                                                                                                              22;
                                                                                                                                                           Score 144;
Pred. No. 9.
                                                                                                                                                 Mismatches
                                                                                                                                                 DB 21;
9.5e-09;
hes 61;
                                                                                                                                                                        Length 130;
                                                                                                                                                  Indels
                                                                                                                                                  6;
                                                                                                                                                  Gaps
                                                                                                    62
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Qy Qy

Qy Db

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YANGA MARANTAN MARANT
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                                                                                                                     30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid excretion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B01786;
(AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                            17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli; yahN gene; amino acid production; excretion protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                     98RU-0124016.
99RU-0104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the YahN amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                       E. coli; yfiK gene;
amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
           Tokhmakova IL;
                      Livshits VA,
                                          (AJIN ) AJINOMOTO CO INC
                                                               30-DEC-1998;
09-MAR-1999;
                                                                                                  17-DEC-1999;
                                                                                                                       05-JUL-2000
                                                                                                                                             EP1016710-A2
                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                      Escherichia coli YfiK amino acid excretion
                                                                                                                                                                                                                                             03-JAN-2001
                                                                                                                                                                                                                                                                  B01788;
                                                                                                                                                                                                                                                                                       B01788 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                              191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTLEWWFAYLLT---SIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW 57
                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                      glitdlsnpqtvlffisifsvtlnaetptwarlmawagivlasiiwrvflsqafslpavr
                                                                                                                                                                                                                                                                                                                                                                                                                                glfglatlitqceeifslirivggayllwfawcsmrrqstpqmstlqqpisapwyvffrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         itmdplhavyltvglfvitffnpganlfvvvqtslasgrra-gvltglgvalgdafysgl\\
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                                                                                                                                                                                                                                                                                                                                           ray----grmqrvasrvigai 207
                                                                                                                                                                                                                                                                                                                                                                IALWIKGPKQMKALNKIFGSL
                                                                                                                                                                                                                                                                                                                                                                                                           AVEVNLTNPKSIVFLAALFPQFIMPQQP---QLMQYIVLGVTTIVVDIIVMIGYATLAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R--GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRH--LFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                       excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                            (first entry)
                     Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zakataeva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĀ,
                                                               98RU-0124016
99RU-0104431
                                                                                                99EP-0125263
                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29pp;
                                                                                                                                                                                      amino acid
n protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΝP,
                                                                                                                                                                                                                                                                                        195
                                                                                                                                                                                                                                                                                                                                                                  191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126.5; DB 21
Pred. No. 1.9e-06;
8; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakanishi K,
                    Nakanishi K,
                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                               production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                     Aleshin VV,
                                                                                                                                                                                                 excretion
                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aleshin
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                     Troshin
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                                                                                                                                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                      Pγ
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RESULT
B11637
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the YfIK amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used
                                                                                                                                                                                                                                                                                                                                в11637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copies of its gene are transfected into is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
New protein from Agrobacterium vitis, useful
                          N-PSDB;
                                                                                                                                                                                                                                  stress
                                                                                                                                                                                                                                             Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer;
                                                                                                                                                                                                                                                                                A. vitis hypersensitive response elicitor protein,
                                                                                                                                                                                                                                                                                                        23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                        B11637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                            06-NOV-1998;
                                                                                                                                   05-NOV-1999;
                                                                                                                                                           18-MAY-2000
                                                                                                                                                                                                          Agrobacterium vitis
                                                                                                                                                                                   WO200028056-A2
                                                                                   (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                   162
                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 alqfvnvkiilygvtalstfvlp-qtqalswvv-gvsv----llamig--tfgn--vcwa 161
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                         2000-376567/32
)B; A61502.
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                                                            ŢĮ,
                                                                                                                                                                                                                                                                                                                                                                                                                 laghlfqrlfrqygrqlnivlall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVGTLFSRSVI---AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              afwtytlitamtpgpnnilalssatshgf----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR------
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)B; A52690.
                                                                                                                                                                                                                                                                                                                                                                                                                                        KGPKQMKALNKIFGSLFMLVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVNLTNPKSIVELAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWI 175
                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                  resistance; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                             Herlache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; ilarity 24.5%; Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                           98US-0107387.
                                                                                                                                    99WO-US26079
                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29pp; English.
                                                              TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of L-amino acids by an the expression amount of
                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 126; DB 21;
Pred. No. 1.8e-06;
6; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                                                                                  plant
                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                              Н;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of an L-amino acid exc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rqstrvlagmslgflivmll
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                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                   NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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e.g.

for imparting

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RESULT
Y99598
ID Y9
XX
Y9
AC Y9
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AC Y9
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CHICLE
AC Y9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences B11630-B11688 represent proteins from Agrobacterium vitis which clicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (A61501-A61524) encoding the A. vitis HR CC elicitor proteins. The HR is a rapid, localised necrosis that is coccurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in con-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death component on the component of pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death component on the component of pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death component on the component of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria control insects, to impart resistance to environmental stresses, e.g., cold, and to import entitional value, e.g., altered oil content. The control insects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of control of previously untreatable diseases; provide systemic treatment; can heaminals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЪ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             E. coli L-threonine resistance protein, RhtC
                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-2000
                                                                                                    EP1013765-A1
                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                   L-homoserine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      а
                                  28-JUN-2000
                                                                                                                                                                                                                                                                  L-threonine resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y99598 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance to disease or stress to plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 WIKGPKOMKALNKIFGSLFMLVGALLASA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTLFSRSVI-----AFEVLKWAGAAYLIWLGI-QQWRAAGAIDLKSLASTQSRRHLFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liasitwlavlspgadfamvsrnsflygrksglaasmgiaiacw------fhvi
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                   L-valine;
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                                                                                                                                                                                                                                                           L-threonine synthesis; rhtC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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Pred. No. 4.4e-06;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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     17-DEC-1999;
                                                             05-JUL-2000
                                                                                                                                                                                                                                 E. coli; yggA gene; amino acid production;
amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise
                                                                                                                  EP1016710-A2
                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                Escherichia coli YggA amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  B01789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B01789 standard; Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the L-threonine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 15-16; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Escherichia bacterium having enhanced L-threonine resistance to enhanced RhtC protein activity, used to produce L-threonine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-homoserine, L-valine and L-leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 ATLAQRIALWIKGPKQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LTSIILTLSPGSGAINTMTTSLNHGYPAG-----GVYCWASDRTGDSYCAGWRGVGTLFS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrgyqrlakwidg-----fagalfagfgihliisr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kglltnlanpkaiiyfgsvfslfvgdnvgttarwgifaliivetlawftvvaslfalpqm 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hlii--ekmawlhtlimvggglylcwmgyqmlr--galkkeavsapapqvelaksgrsfl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSVIAFEVLKW-----AGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHL-----FQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mvhivalmspgpdfffvsqtavsrsrkeammgvlgitcgv-----mvwagiallgl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-414602/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A48443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zakataeva
     99EP-0125263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98RU-0123511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-0125406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%;
21.0%;
                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΝP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 122; DB 21;
Pred. No. 5.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aleshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Belareva AV,
                                                                                                                                                                                                                                                        excretion
                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                        protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIVVDIIVMIGY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tokhmakova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL;
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PRANCE PRODUCTION OF THE PRANCE PRODUCTION OF THE PRODUCTION OF TH

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Matches
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Best Local
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                                                                                                                                                                                                                                                   C. glutamicum Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                    Corynebacterium
                                                                                                                                                                                                                                                                                      12-MAR-1998
                                                                                                                                                                                                                                                                                                                      W37715;
                                                                                                                                                                                                                                                                                                                                                      W37715 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 25; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; A52691
                                                                                                                                  DE19548222-A1
                                                                                                                                                                                                      Microbial
                                                                                                                                                                                                                   LysG; LysE; ORF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO CO INC
 (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH
                                   22-DEC-1995;
                                                                 22-DEC-1995;
                                                                                                 26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ALWIKGPKOMKALNKIFGSLFMLVGALLA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLAST----QSRRHLFQRAV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAY-----LLTSIILTLSPGSGAINTMTTSLNHGYPAG-GVYCWASDRTGDSYCAGWRG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                        aprlrtakagriinlvvgcvmwfialgla 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          avtwlnphvyldtfvvlgslggq--ldvepk--rwfalg--tisasflwffglallaawl 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVNLTNP----KSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gsallmqspwllalvtwggvafllwygfgafktamssnie-lasaevmkqgrwkilatml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fsyyfgglalgaamilplgpqnafv--mnqgirrqyhimiallcaisdlv--licagifg 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-414802/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                    production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98RU-0124016
99RU-0104431
                                 95DE-1048222
                                                                 95DE-1048222
                                                                                                                                                                    glutamicum
                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                lysine transport; regulatory protein; export protein; ion; amino acid; animal feed additive.
                                                                                                                                                                                                                                               E protein (lysine export protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113; DB 21;
Pred. No. 6.2e-05;
6; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakanishi
                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aleshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Troshin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
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 Q_{\underline{Y}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ОĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
Y04104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the LysE protein product, a lysine export protein. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
fructotransferase
                Levan fructotransferase
                                                                                                                                 28-AUG-1997;
                                                                                                                                                                                                                                    JP11069978-A
                                                                                                                                                                                                                                                                    Arthrobacter nicotinovorans
                                                                                                                                                                                                                                                                                                     Arthrobacter
                                                                                                                                                                                                                                                                                                                                     Arthrobacter
                                                                                                                                                                                                                                                                                                                                                                                                        Y04104;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Y04104 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 42; Page 10; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-333867/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eggeling L,
                                                                                                 (NIOC ) NIPPON OIL CO
                                                                                                                                                                    28-AUG-1997;
                                                                                                                                                                                                    16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                       10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 PKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWIK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LEWWFAYLLTSIILTLSPGSGAINTMTTSL-NHGYPAGGVYCWASDRTGDSYCAGWRGVG
                                                1999-247463/21
DB; X19826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kvea-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          llsnaapivldimrwggiayllwfavmaakda--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLEQRAVEVNLTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                   nicotinovorans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sahm H,
                                                                                                                                                                                                                                                                                                                                     nicotinovorans levan fructotransferase protein
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                  97JP-0232421
                                                                                                                                                                    97JP-0232421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -pqileeteptvpddtplggsavatdtrnrvrvevsvdkgrvwvk 144
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                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                          484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89.5; D
Pred. No. 0.03
25; Mismatches
                                                                                                                                                                                                                                                                                                     levan
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                  for
                recombinant production of levan
                                                                                                                                                                                                                                                                                                       fructotransferase
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DB 18; 79;

Indels Length 236;

35;

Gaps 61 61

4.

96

RESULT W37715

PAN XXX

Qy ДЪ Q Вb Ωy В

В

Length 517;

Indels

56;

Gaps

7;

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RESULT 14
Y04105
XX
Y04105
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Y04105
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Y04105
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I8-AUG
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X
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                                           The present sequence represents Arthrobacter nicotinovorans levan fructotransferase. The present invention also describes a method for the preparation of levan fructotransferase in which a transformant is cultured in a medium and levan fructotransferase is collected from the culture. The method can prepare levan fructotransferase in a
                                                                                                                                                                                            Claim 3; Page 8-9; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11069978-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arthrobacter nicotinovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arthrobacter nicotinovorans levan fructotransferase protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y04105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents Arthrobacter nicotinovorans levan fructortansferase. The present invention also describes a method for the preparation of levan fructotransferase in which a transformant is cultured in a medium and levan fructotransferase is collected from the culture. The method can prepare levan fructotransferase in a
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                                                                                                                                                                                                                                                                   Levan fructotransferase gene - for recombinant production of levan
                                                                                                                                                                                                                                                                                                                       WPI; 1999-247463/21
N-PSDB; X19827.
                                                                                                                                                                                                                                                                                                                                                                                           (NIOC ) NIPPON OIL CO
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arthrobacter nicotinovorans;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y04105 standard; Protein; 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQLMQ-YIVLGVTTIVVDIIVMIGYATLAQRI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPAGGVYC-----WASDRTGDSYCAGWRGVGTLFSRSVIAFEVLKWAGAAYLIW 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ldi-swdtaanvgvsvgrssdgsrhtnigkygdelyvdrassegsgyalapytraaapid 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ldwgwdwyaavtwpaveapetkrlatawmnnwkyaarnvptdasdgyngqnsitrelrle 31:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 AA;
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19.3%; Pred. No. 1.1;
ative 34; Mismatches
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Y38701
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Best Local Similarity
Matches 41; Conser
             Amino acid sequences Y38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFS) Z11972-Z1238. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
                                                                                                                                                                                                                                          Claim 4; Page 252; 524pp; English.
                                                                                                                                                                                                                                                                                   Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection {\sf C}
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-327407/27.
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06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae antigen encoded by partial ORF104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 anarsvhlrifvdtqsvevfvnsghtvvsqqv 485
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                                                                                                                                                                                                                                                                                                                                                                                                              G, Masignani V,
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97GB-0023516.
97GB-0024190.
97GB-0024186.
97GB-0025158.
97GB-0026147.
98GB-0000759.
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19.3%; Pred. No. 1.2;
tive 34; Mismatches
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27, Appl
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e 5, Appl
e 5, Appl
e 5, Appl
e 6, Appl
e 7, Appl
e 7, Appl
e 7, Appl
e 8, Appl
e 9, Appl
e 15, A

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Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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(without alignments)
182.410 Million cell updates/sec
US-08-232-537-2
US-08-358-171-2
US-09-09-947-2
US-08-468-812-2
US-08-863-102-1
US-08-863-102-4
US-08-863-102-4
US-08-802-141-4
US-08-8726-214-10
US-08-973-674-18
US-09-073-674-18
US-08-474-659-34
US-08-474-651-377-34
US-08-611-977-34
US-08-752-307B-3
US-08-752-307B-3
US-08-752-307B-3
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US-08-752-307B-3
US-08-752-307B-3
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5432081-9

US-08-875-223-8

US-08-448-603A-30

US-09-134-075-30

5432081-7
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5474933-4
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                                                                                                                                                                                                                                                      Sequence 7, Appli
patent No. 5474933
Sequence 24, Appl
Patent No. 5432081
Sequence 8, Appli
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
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14, Appli
18, Appli
 Appl
Appl
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Appl
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-254-7
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US-08-476-254-7
; Sequence 7, Applica
; Patent No. 5846531
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                                                                                Query Match
Best Local S
Matches 38
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                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1400 K STREET NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-2477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                  TELEFAX: 202 628-8034
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
34
39
39
                                                                                                                                                                                                                                                                                          FILING LASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, JAMES A.
NAME: POULOS III, JAMES A.
171, 174
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,254
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WEINER, RONALD M.
APPLICANT: FUQÜA, WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: WATSON COLE STEVENS DAVIS, P.L.L.C.
STREET: 1400 K STREET NW
                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
    99
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                              WMMVGELAGVALVAIAAVMGVASMMLNYPQLFDILKWVGGLYLGYIGISMWRAKGKMANL 77
    KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                   38; Conser
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                                                                                   Conservative
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US-08-687-352-21
US-08-08-368-071-10
US-08-458-181-10
US-08-458-181-10
US-08-793-02172-10
US-07-959-943-7
US-07-873-985-12
US-07-762-298-2
US-08-73-98-2
US-08-73-98-89
US-08-637-7598-89
US-08-637-7598-89
US-08-700-0138-15
                                                                                   21;
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                                                                                 Score 155; DB 2;
Pred. No. 1.2e-10;
1; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                              Version
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                                                                                                          Length 153;
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Patent No.
Sequence
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Result No.

Score

Match Query

Length

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212252222213133231163246

Gaps

2;

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Searched:

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.

Post-processing: Minimum Match 0%

Database

Issued_Patents_AA:*

Title: Perfect score:

protein -

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; TYPE: PRT; ORGANISM: L. US-09-068-195-24
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APPLICANT: EINER, RONALD M.; FUQUA JR., WILLIAM
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Patent No. 6140078
                                                            SEQ ID NO 24
LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                 TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid TITLE OF INVENTION: Bacterium, and Its Use in a Lacctic Acid Bacterium for INVENTION: Production of Desired Protein
FILE REFERENCE: Sanders-60113/0252227
CURRENT APPLICATION NUMBER: US/09/068,195B
CURRENT FILLING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: PCT/EP97/04755
EARLIER FILLING DATE: 1997-08-20
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER FILLING DATE: 1997-03-13
EARLIER FILLING DATE: 1997-03-13
EARLIER FILLING DATE: 1996-09-05
NUMBER: EP 96202444/4
EARLIER FILLING DATE: 1996-09-05
NUMBER: EP 96202444/4
EARLIER FILLING DATE: 1996-09-05
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sanders, Jan W.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
                                                                                                        SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/OFFILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 FSMLAYAS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 FSMLAYAS 145
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nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: 496,804
FILING DATE: 21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 KSLASTQSRRHLEQRAVEVNLTNPKSIVFLAALEPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 WMMVGELAGVALVAIAAVMGVASMMLNYPQLEDILKWVGGLYLGYIGISMWRAKGKMANL 77
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                       lactis MG1363
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Pred. No. 1.2e-10;
""cmatches 51;
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RESULT 5
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5432081-9
; Patent No. 5432081
; APPLICANT: JEFFERSON, RICHARD A.
; TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLI
;GLUCORONIDE PERMEASE GENE
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FILING DATE: 10-NOV-1987
SEQ ID NO:9:
LENGTH: 428
                                                                               Sequence 8, Application US/08875223 Patent No. 6127175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VIGNE, Emmanuelle
APPLICANT: PERRICAUDET, Michel
APPLICANT: DEDIEU, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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FILING DATE: 15-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 447,976
FILING DATE: 08-DEC-1989
APPLICATION UMBER: 264,586
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF
                                                                                                                                                                                                 188 YFICFKSTRENVVRIVAQPSLNISLQTLKRNRPLFMLCIGAL 229
                                                                                                                                                                                                                                       164 Y----ATLAQRIALWIKGPKQMKALNKIFGS--LFML-VGAL 198
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                                                                                                                                                                                                                                                                                                                                                           73 LLFGTAPLMIFSVLVFWVLTDWSHGSKVVYAYLTYMGLGLCYSLVNIPYGSLATAMTQQP 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD--RTGDSYCA-GWR----- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 YLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGTLFSR--
                                                                                                                                                                                                                                                                                                              QSRRHL-FQRAVEVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIG 163
                                                                                                                                                                                                                                                                                                                                                                                          ---GVGTLFSRSVIAFEVL-KWAGA-----AYLIWLGIQQWRAAGAIDLKSLAST----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTQRTAKLVKAGFVVGIVIPSVILFGLAAAY--FIGGNPIEIPINSHAFVPDFSQ-----
                                                                                                                                                                                                                                                                             QSRARLGAARGIAASLT----FVCLAFLIGPSIKNSSPEEM-VSVYHFXTIVLAIAGMVL 187
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58; Conserv
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21.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /08/138,546
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Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 428;
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US-08-448-603A-30
Sequence 30, Application US/08448603A
Patent No. 5864027
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
APPLICANT: Makamura, Gerald R.
APPLICANT: HIV Envelope 1
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Best Local S
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FR WO FR9 ETLING DATE: 19-JAN-1996 ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Faul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/00747
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06532
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PROST, Edouard
TITLE OF INVENTION: CELLS FOR THE
TITLE OF INVENTION: ADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/10541
FILING DATE: 08-5EP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                         346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UP
ZIP: 19426
                                                                                                                                                                                                                              84 WLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALF 132
                                                                                                                                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/875,223
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                                                                                                                                                                                                                                                                         IDIMTSMMIHGYESWALHCHCSS-PGSLQCIAGGQVLASWF-RMVV------DGAMF--
                                                                                                                                                                                                                                                                                                            INTMTTSLNHGYPAGGVYCWASDRTGDSYC-AGWRGVGTLFSRSVIAFEVLKWAGAAYLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 amino acids
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VENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                            6.5%; pred. No. 1.
23.9%; pred. No. 1.
-+ive 21; Mismatches
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HIV Envelope Polypeptides
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                                                                                                                                                                                                       Sequence 30, Application US/09134075 Patent No. 6042836
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                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
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APPLICATION NUMBER: 08/0:
FILING DATE: 07-JUN-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                           APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
                                                                                                                                                                                                                                                                                                                                                                                              527
                                                                                                                                                                                                                                                                                                                                                                                                                                123 KSIVFLAA------LFPQFIMPQ-------PPQLMQYIVLGVTTIVVDIIVMIG 163
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                     STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: 01
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              AGSTMGAASITLTVQARLLLSGIVQQQNNLLRAIEAQQHLLQLIVWGIKQLQARVLAVER 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEVIKWAGAAYLIWIGIQQWRAAGAIDLKSLASTQSRRHLFQR-----AVFVNLTNP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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19.5%; Pred. No. 19;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                        ; Patent No. 5432081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-075-30
                                  SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.5%; Score 68.5; Best Local Similarity 19.5%; Pred. No. 19; Matches 43; Conservative 28; Mismatches
                                                    NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/13:
FILING DATE: 15-OCT-1993
PRIOR APPLICATION NUMBER: 447,976
APPLICATION NUMBER: 447,976
ETLING DATE: 08-DEC-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
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LENGTH: 857 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
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NAME: Haliday, Emily
REGISTRATION NUMBER: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 YATLAQRIALWIKGPKQM------KALNKIFGSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                          587 YLRDQQLLGIWGCSGKLICTTSVPWNASWSNKSLDKIWDNM 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 IEPL------GVAPTKAKRRVVQREKRAVGIGAVFLGFLGA 526
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                   LENGTH: 456
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                      Query Match
Best Local Similarity 18.6
Conservative
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Best Local Similarity 26.1%;
Matches 58; Conservative 2
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APPLICANT: Peery,
APPLICANT: Skatru
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 317-276-1917
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: 921
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317,276-2459
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1302 amino aci
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: AUREOBASIDIUM PULLULANS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                            811 MQWFSGQSVPSLMSSLSSDAGQL-----
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                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 LLFGTAPLMIFSVLVFWVLTDWSHGSKVVYAYLTYMGLGLCYSLVNIPYGSLATAMTQQP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                 3 LEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD--RTGDSYCA-GWR----- 58
LF-----SRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSR-RHLFQRAV 115 : | | : | | : | | : | | : | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFICFKSTRENVVRIVAQPSLNISLQTLKRNRPLFMLCIGAL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSRRHL-FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GVGTLFSRSVIAFEVL-KWAGA-----AYLIWLGIQQWRAAGAIDLKSLAST----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAFAMGALFL-LSYYTDVAGVGAAARAHAVTGAGIRCLRRRLCRTSGGQCEYRWGKFRPF 80
                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                     1302 amino acids
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                                                                                                                                                                                                                                                                                  Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                           6.4%; Score 67.5;
18.6%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/232,537
                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 68; DB 6; Le; Pred. No. 9.2; 27; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                              X9212
                                                                                                                                          Mismatches
                                                                                                                                                                          DB 1; Length 1302;
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                                                                                                                                        Indels
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                                                            ---ACLSGVAIGT 843
                                                                                                                                        73;
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                                                                                                                                        Gaps
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US-08-358-171-2
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Best Local S
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: ALL TRANS
TITLE OF INVENTION: ENCODING
THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF TH
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REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-28-5197
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                             104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 IFTVCVSITGGIILAHVVAWKIAVVLL-AAVPVMITAGYVRLRVLALAESRHRSAYNDAA 902
                                                                                                                                                                                                                                104 ---TQSRRHLEQRAVEVNLTNPKSIVELAALEPQEIMPQQPQLMQYIVLG-----VTTI 154
                                 215 LPARTILLGWGPYALLYLYATIADATSISPKLQMVPALIAKAVPTVNAMNYALGS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-DEC CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 LTSIILTLSPGSGAINTM---TTSLNHGYPAGGVYCWASDRTGDSYCAGWRG----VGTL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                          CSSAAVAWGRYHHFCTRSRLDWNTAVSLVFFVWLSSAFWAALPLLGWGHYDYEPLGTCCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                              LLVLSLALADSGISLNALVAATSSLLRRWPYGSEGCQAH------GFQGFVTALASI 103
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                                                                                                   VVDIIVMIG-----YATLAQRI---
                                                                                                                                                                 LDYSRGDRN-FTSFLF-----TMAFFNFLLPLFITVVSYRLMEQ-KLGKTSRPPVNTV
                                                                                                                                                                                                                                                                                                                                                                            FSRSVIAF-----EVLKWAGA---AYLIWLGIQQWRAA----GAIDLKSLAS--- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 6.3%; Score 66.5; D
Similarity 21.7%; Pred. No. 7.4;
51; Conservative 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 amino acids
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FONG, Henry K.W.

VENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN,

VENTION: ENCODING SAME, AND ANTIBODIES THERETO
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                                                                                               -----ALWIKGPKQMKALNKIFGS 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 291;
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                         Sequence 2, Application US/08468812 Patent No. 5935836 GENERAL INFORMATION:
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APPLICANT:
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; MOLECULE TYPE: protein US-09-090-947-2
RESULT 12
US-08-468-812-2
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Patent No. 6008338
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acid
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                              215 LPARTLLLGWGPYALLYLYATIADATSISPKLQMVPALIAKAVPTVNAMNYALGS
                                                                                                                       155 VVDIIVMIG------YATLAQRI-----ALWIKGPKQMKALNKIFGS 190
                                                                                                                                                                                                                                             104 CSSAAVAWGRYHHFCTRSRLDWNTAVSLVFFVWLSSAFWAALPLLGWGHYDYEPLGTCCT 163
                                                                                                                                                              164 LDYSRGDRN-FTSFLF-----TMAFFNFLLPLFITVVSYRLMEQ-KLGKTSRPPVNTV
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                                                                                                                                                                                                                                                                                                                                                                  11 LTSIILTLSPGSGAINTM~--TTSLNHGYPAGGVYCWASDRTGDSYCAGWRG----VGTL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/090,947
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                                                                                                                                                                                                 ---TQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLG-----VTTI 154
                                                                                                                                                                                                                                                                                  FSRSVIAF-----EVLKWAGA---AYLIWLGIQQWRAA-----GAIDLKSLAS--- 103
                                                                                                                                                                                                                                                                                                                             LLVLSLALADSGISLNALVAATSSLLRRWPYGSEGCQAH------GFQGFVTALASI 103
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%;
21.7%;
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Pred. No. 7.4;
5; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 291;
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Vehmaanper , Jari

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RESULT 13
US-08-863-102-1
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                                                                                                 Sequence 1, Application US/08863102
Patent No. 6015828
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
         GENERAL INFORMATION:
APPLICANT: Cuppoletti, John
TITLE OF INVENTION: Chemical Modification of
TITLE OF INVENTION: Chloride Channels as a Treatment
TITLE OF INVENTION: Fiobrosis and Other Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-UUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INCOMMATION:
NAME: Bugaisky, Larry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bugaisky, Larry B. 8. REGISTRATION NUMBER: 35,086 REFERENCE/DOCKET NUMBER: 10. TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Relicion DATA: CURRENT APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/332,412
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                         88 GNEVAGKGWSTGGRRTVTYNASENPSGNGYLTLYGWTRNPLVEYYIVESW 137
                                                                                                                                                                                                                                         61 GTLFS------RSVIAFEVLKWAGAAYLIWLG-----IQQW 90
                                                                                                                                                                                                                                                                            28 LALAIAGALLPGTAHADTTITQNQTGYDNGYFYSFWTDAPGTVSMTLHSGGSYSTSWRNT 87
                                                                                                                                                                                                                                                                                                              10 LLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD------RTGDSYCAGWRGV 60
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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Lahtinen, Tarja
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Fagerstr m, Richard
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22.7%;
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Pred. No. 9.3;
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                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                              Length 344;
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RESULT 14
US-08-863-102-4
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US-08-863-102-1
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                 Sequence 4, Application US/08863102 Patent No. 6015828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM_PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,102
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (513) 977-8141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                    APPLICANT: Cuppoletti, John TITLE OF INVENTION: Chemical TITLE OF INVENTION: Chloride TITLE OF INVENTION: Fiobrosi NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 45202
COMPUTER READABLE FORM:
                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 MALVSWAMDYAIAACLQAQQWM-SRGLNTNLLLQYLAWVTYPVVLITFSAGFTQILAPQA 162
ADDRESSEE: Jackie A. Zurcher,
ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street,
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 VGSGIPE-MKTILRGVVLKEYLTLKTFVAKVIGLTCALGSGMPLGKEGPFVHIASMCAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Jackie A. Zurcher,
ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street,
STREET: 1900 Chemed Center
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Zurcher, J. A. REGISTRATION NUMBER: 42,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QWRAAGAIDLKSLASTQSRRHLFQRAVFVNL-----TNPKSIVFLAALFPQFIMPQQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PQLMQYIVLGVT-----TIVVDIIVMIGY-ATLAQRIALWIKGP-----KQMKAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPEPWRSPPSPRTPPELLEYGQSRCARCRMCSVRCHKFLVSRVGEDW----IFLVLLGLL 103
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                                                                                                                                                                                    Chemical Modification of Chloride Channels as a Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
25.0%;
                                                                                                                                                                Fiobrosis and Other Diseases
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Pred. No. 35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett

Diskette, 3.5 inch

COUNTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                             US-08-802-141-4
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Best Local Similarity 25.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08802141
Patent No. 5773009
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (513) 977-8141 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/863,102
FILING DATE: 23-MAX-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A.
REGISTRATION NUMBER: 42,251
REGISTRATION NUMBER: 42,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (513) 977-8377
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                         TITLE OF INVENTION: ROTAVIRUS STRAIN AND RELATED TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: ami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 LSKFLSLF 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 QWRAAGAIDLKSLASTQSRRHLEQRAVEVNL-----TNPKSIVFLAALEPQFIMPQQ 140
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                                                                                                              COUNTRY:
                                                                                                                                                                    STREET:
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                                                                                              30303
                                                                                                                                              Atlanta
                                                                                                              Georgia
Y: USA
                                                                                                                                                                                                                                                                              GLASS, ROGER I.
GENTSCH, JOHN R.
BHAN, M. K.
DAS, BIMAL K.
                                                                                                                                                                    127 Peachtree Street, Suite 1200
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Pred. No. 35;
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-802-141-4
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Search completed: May
Job time: 414 sec
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 688-9880
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/231
PAPPLICATION NUMBER: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,01
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,141
FILING DATE: 19-FEB-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                138 -KFVDYFKT----
                                                                                                                                                                                                                                                                          102 WMFTYL---VLPNTAQTSVVVNVMNETVN-----ISIDNSGSAY------ 137
                                                                                                                                                                                122 -----
                                                                                 238 SYAVRSQRIA 247
                                                                                                                 163 GYATLAQRIA 172
                                                                                                                                            180 SDAYGDLRVGTYFNPVPNAVINLNADF--YVIPDSQQEMCTEYIRRGLPAIQTTTYVTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 40.,
TELEPHONE: 688-9880
                                                                                                                                                                                                                                          65 SRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTN--- 121
                                                                                                                                                                                                                                                                                                         5 WWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGTLF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                      2001, 14:39:23
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Pred. No.
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9b_ba2:AP003004

9b_ba2:AP003012

9b_ba1:AE004372

9b_ba1:AE004786

9b_ba1:AE005402

9b_ba1:AB024601

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9b_ba1:AB063272
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gb_htg7: AC020874
gb_htg11: AC026742
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gb_htg7:AC020833
gb_ba2:AP003001
gb_ba2:AP003001
gb_ba2:AP003005
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gb_ba2:BF003014
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9b_ba2:D90823

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9b_ba1:AE004221
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gb_ba1:AE000458
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Database length: -1216004940
Search time (sec): 1745.950000
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Sequence
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Query length: 205
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gb_ba1:AE004937
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-DB=-GenEmbl -ORMT=fastap -SUFFTX=rge -GAPOP=12 000 -GAPEXT=4.000
-MINMATCH=0.100 -COOPCL=0.000 -LOOPEXT=0.000 -GGAPOP=4.500
-QGAPEXT=0.050 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_GENEPORT -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09466935_@CGN1_1_5396 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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      9.1e-08

9.0e-07

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1.6e-09

5.1e-07
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8.0e-13
1.9e-13
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7.6e-65
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3.0e-96
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.3e-09
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.4e-72
1401 i AEO0421 vibrio cholerae chrc
338579 i APO03004 Mesorhizobium loti
34647 i APO03012 Mesorhizobium loti
10176 i AEO04372 Vibrio cholerae chrc
10235 i AEO04786 pseudomonas aeruginc
11313 i AEO05402 Escherichia coll O15
14807 i ABO24601 pseudomonas aeruginc
111000 i Continuation (21 of 28) of
720 i ARO63272 Sequence 6 from patent
885 i X67020 S.colwelliana mlgA gene.
96231 i AF188935 Bacillus anthracis p
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6373 i AC020870 Mus muscullus clone
6373 i AC020877 Homo sapiens chromose
638 i AC022157 Homo sapiens chromose
6396 i AC020970 Mus muscullus clone
6378 i AC020874 Mus muscullus clone
6379 i AE004104 Vibrio cholerae chro
6370 i AE004937 Pseudomonas aeruginc
6371 i AE004937 Pseudomonas radiodur
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gb_ba3:PACARAB
gb_ba3:PAU81259
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AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
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Align seg 1/1 to: AX030175
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                                                                                                                                                                                                                                                                                                    557 ATGACCTTAGAATGGTGGTTTGCCTACCTGCTGACATCGATCATTTTAAC
                                                                                                                                                  34 isGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGly
                                                                                                                                                                                                                                    17 rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1061.00
Ratio: 5.176
Similarity: 100.000
                                                              AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe 67
rValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleT
                                                                                                                              ACGGTTATCCGGCCGGTGGCGTCTATTGCTGGGCTTCAGACCGGACTGGC
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Belareva, A.V., Aleshin, V.V., Livshits, V.A.,
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Escherichia coli
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/db_xref="GI:1019033"
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/translation="MILEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCW
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STQSRHILFQRAVFVNLTNPKSIVFLAALFPQFIMPQOPQLMQYIVLGVTTIVVDIIV
MIGYAFLAQRIALMFKGFKOMKAKLFGSLFMLVGALLASARHA"
a 319 c 311 g 310 t
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/db_xref="taxon:562"
557. .1174
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i AE004079 Xylella fastidios
i U04992 Pseudomonas aerugino
i U81259 Pseudomonas aerugino
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Direct Submission
Submitted (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu; Phone: 608-262-2534; Fax:
                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 91414)
Plunkett,G. III., Burland,V., Daniels,D.L. at
Analysis of the Escherichia coli genome. III
region from 87.2 to 89.2 minutes
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels, D.L., Plunkett, G. III., Burland, Nanalysis of the Escherichia coli genome: from 84.5 to 86.5 minutes
Science 257 (5071), 771-778 (1992)
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                                                                                                                  A new family of peptidyl-prolyl isomerases Trends Biochem. Sci. 20 (1), 12-14 (1995)
                                                                                                                                                         Rudd, K.E., So
Rouviere, P.E.
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Nucleic Acids Res. 21 (23), 5408-5417 (1993)
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                                                                     Daniels, D.L
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On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. The entire sequence was independently determined from E. coli MG1665. Overlaps and conflicts with other sequence determinations are annotated. Reference [1] describes the original sequence determination of a 91408 bp sequence. References [2], [3], and [4] describe subsequent corrections and/or updates to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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/clone_lib="lambda library of Daniels and Blattner"
/more="pl 1 at 3974 kb; 84.7 minutes"
/note="This sequence comprises the following lambda clones: DD850(EC15-116), DD851(EC13xM4), DD854(EC15-177), DD856(EC19xM8.1), DD858(EC17xM9), DD856(EC17-221), DD864(EC27-149), DD865(EC21-76), DD867(EC27-860). Ml3mp19 or Janus vectors were used for
                                                                                                                                                                                                              complement(703. .1104)
/gene="f133"
                                                                                                                                                                                                                                                              586. .724
/note="predicted bend of
                                                                                                                                                                                                                                                                                                                             /translation="mahtsrhnefsigasaslwecmlnqwlgrlyqnqdahtglqfea
RIAQRQSLVKQLHERQLDLLITTEAPKMDEFSSQLLGYFTLALYTSAPSKLKGDLNYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(266.
/gene="f198"
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177. .205
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                                                                                                                                                                      complement(703. .1104)
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/gene="f198"
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                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA67566.1"
/db_xref="GI:148170"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted
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/note="CGSC
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/note="CGSC No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="clone EC15-116"
                                                                                                                                  /codon_start=]
                                                                                                                                                    note="CGSC No. 18010;
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.862)
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CDS gene

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                      /note="V00290; 1
3458. .3556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="unknown"
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GEGCLIADHLQAVCAFLEGKHALEXFKPTDAVSRALQHDLSDVIGQEQKKRGLEITAA
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RSPHHSASLTAMVGGGAIPGPGISIAHNGVLFLDELPEFERTLDALREPIESGQIH
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/gene="ilvG"
/note="CGSC No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1585. .3135)
/gene="f516"
/note="similar to Mg ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAESFTTTNRYFDNKHYPRGFSRHGDFTIKEAQLLERHGYAFNELDLGKREPVTEEEKLFVAVCRGEREPVTEAERVWSKYMTRIKRPKRFHTLSAVNRRLKVLKTTPILTINKKGEMPFFYVSSFCRWMSKRSIAR"
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1223, .1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="promoter matrix score of 1151. .1179
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/transla+:-- "
                                                                                                                                                                                                                                                                                                                                                                                               /note="corresponds 3379. .5721
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3336. .3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="promoter matrix score of 74"
3336. .3676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted bend of 79 3297. .3326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsulata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="terminator-like complement(1585. .3135)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="corresponds 3336. .12791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="f516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="0137"
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/db_xref="GI:148175"
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3696. .4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDAMWLEGTLIHLGLSIRAWQRLLKVARTIADIDQSDIITRQHLQEAVSYRAIDRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRTRAKITYPARFOLVAAMNPSPTGHYQGNHNRCTPEQTLRYLNRLSGPFLDRFDLS
LEIPLPPPGILSKTVVPGESSATVKQRVMAARERQFKRONKLNAWLDSPEIRQFCKLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHLQKLLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                        /gene="ilvL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3433
                                                                                                                                                                  LlvG"
                                                                                                                                                                                                                                                                                                                                               lvL"
                                                                                                                                                                                                                                                                                                                                                                              ECILVX(1. .2343)"
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                                                                                                                                                                                                                                                                                                                                                                                                                  .9456)"
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                                                                                                          E. coli K12"
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alignment_block:
US-09-466-935-2 x ECOUW85/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62011 CGATTCATATTGTGCTGGGTTGGGGGTTGGGACGCTATTTTCCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   61861 GCTGGCCTCTACTCAATCGCGTCGACATTTGTTCCAGCGCGCAGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61911 TGGCTGGGAATCCAGCAGTGGCGCGCCGCTGGTGCAATTGACCTTAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61961 CAGTGATTGCGTTTGAAGTGTTGAAGTGGGCAGGCGCGCCTTACTTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGTTATCSCGGCCGGTGGCGTCTATTGCTGGGCTTCAGACCGGACTGG
                    LeuAsnLysIlePheGlySerLeuPheMetLeuValGlyAlaLeuLeuAl 200
                                                                                                                                                                         CGTCACCACTATTGTGGTCGATATTATTGTGATGATCGGTTACGCCACCC
                                                                                                                                                                                                                                                           CAATTCATCATGCCGCAACAGCCGCAACTGATGCAGTATATCGTGCTCGG
                                                                                                                                                                                                                                                                                GlnPheIleMetProGlnGlnProGlnLeuMetGlnTyrIleValLeuGl
                                                                                                                                                                                                                                                                                                                                          rLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSe 100
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CTGAATAAGATTTTCGGCTCGTTGTTTATGCTGGTGGGAGCGCTGTTAGC
                                                                                                        euAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAla 183
                                                                                                                                                                                             yValThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrL
                                                                                  TTGCTCAACGGATTGCTCTATGGATTAAAGGACCAAAGCAGATGAAGGCG
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IQLASGDLEPWFTTVENEVXFPHAEVEQARQMLAKAQKPMLYVGGGVGMAQAVPALRE
FLAATKMPATCTLKGLGAVEADYPYYLGMLGMHGTKAANFAVQECDLLIAVGARFDDR
VTGKLNTFAPHASVIHMDIDPAEMNKLRQAHVALQGDLNALLPALQQPLNQ"
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/gene="0221"
/note="the mutation ilv02096 joins this ORF to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1 replace(4677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restoring function missing in wild-type"
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Identity: 99.029
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                                                                                                                                                                                                                                                                                         AL Submitted (13 °CCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA On Sep 9, 1997 this sequence version replaced 9:1790254.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants H600301 and H601428 (from the Human Genome Project and WGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: markdamber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World wide Web site
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                                                   (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein RNA-encoding) are now designated as gene synonyms instead of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                              Genome Project's World Wide Web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608-263-7459
3 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli K12.
Escherichia coli K12
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Escherichia coli K12 MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608-263-7459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE000458.1
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                                       This should allow
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                            them to be searched for in Entrez as gene
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                                                                                                                                                                                                                                                                                                     3162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RADVQEKFQRDDLQITVATVAFGMGINKPNVRFVVHFDIPRNIESYYQETGRAGRDGL
PAEAKLFYDPADMAWLERCLEEKPQGQUQDIERHKLANAGAFAEAQTCRRLVYLLNYFG
EGROEPCGNCDICLDPRQYDGSTDAQIALSTIGRVKQRFGKGYVVEVYTRGANNQRIE
DYGHDKLKVYGMGRDKSHEHWYSVIRQLIHLGLVTQNIAQHSALQLTEAARPVLAESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQQLEVMTGCRTGQIRLLYIAPERLMLDNFLEHLAHWNPVLLAVDEAHCISQWGHDF
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                            changesN-terminus
SW: P27846)"
                                    'gene 'yay'
/function="orf; Unknown"
/note="ol22; sequence change shortens and
/note="ol22; sequence change shortens and
                                                                                                                                                                                                                                                                                                                              contains
                                                                                                                                                                                                                                                                                                                                                        /note="REP
                                                                                                                                                                                                                                                                                                                                                                                    2104.
                                                                                                                                                                                                                                                                                                                                                                                                           MAEQMPITASEMLSVNGVGMRKLERFGKPFMALIRAHVDGDDEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                       LQLAVPRIVALKPKAMQKSFGGNYDRKLFAKLRKLRKSIADESNVPPYVVFNDATLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ofRECQ_ECOLI SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="enzyme; DNA -
restriction/modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=":
1077. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHDNPFTLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFQLSLAFPLWRGIL
GPNSVLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGY
NHDSNGRSDPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYMGYYQLK
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Phosphorus compounds"
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                                                                                                                                                                                   'note="b3823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="recQ"
/EC_number="3.6.1.-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note='
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MRTLQGWLLPVFMLPMAVYAQEATVKEVHDAPAVRGSIIANMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="pldA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_strain="MG1655"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 950
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                                                                                                                                                                                                                                                                                                                              REP
                                                                                                                                                                                                                                                                                                                        (repetitive extragenic palindromic) element;
REP sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pct identical to 607 amino acids P15043 but has 3 additional N-t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted +1 start at 4003446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted +1 start at 4003392"
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                                                   version (YIGJ_ECOLI
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alignment_block:
                                                                                                                                                                                                        alignment_scores:
                                          Align
                                                                                 US-09-466-935-2 x AE000458/rev
                                                                                                                                             Percent Similarity:
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                                          seg 1/1
MetThrLeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17
                                                                                                                                                                                     Quality:
                                                                                                                                                                  Ratio:
                                            ö
                                        reverse of:
                                                                                                                                                                                                                                                                                                                                                                                      /note="factor & 5426, .5455
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                                                                                                                                                                                                                                                                                                           5438. .5466
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5494. .5523
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RHDRFCGLRTAAGHPVEGGRPLVIKGAYHEILFEKDAMASVALHAIVDFFNRHNSPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="REP (repetitive extragenic palindromic) element; contains 1 REP sequence" complement(3654. .4070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                       1024.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorus compounds"
/note="0340; 99 pct identical amino acid sequence and equal length to PLDB_ECOLI SW: P07000"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="miafevikwagaayliwigiqqwraagaidiksiastqsrrhif
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5526. .6041
/gene="yigL"
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complement(4227. .4254)
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/note="b3824"
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Gaps:
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JOURNAL REFERENCE
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                  seq_documentation_block: LOCUS AE005613
                                                                                                                                           REFERENCE
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                                             I (bases 1 to 10592)

Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                     Escherichia coli 0157:H7.
Escherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                    AE005613 10592 bp I
Escherichia coli 0157:H7
AE005613 AE005174
AE005613.1 GI:12518685
Genome sequence of enterohemorrhagic Escherichia coli O157:H7
Nature 409 (6819), 529-533 (2001)
2 (bases 1 to 10592)
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complement(72. .836)
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complement(72. .836)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="mg2+ transport, system I"
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YCFPTIKSNDNCITKNYLMVINEYPYRNTHIGINDFTEYQLTQENKIEQVFNPHNFKK
                                                                                                                                                                                                                                                                                                                      complement(2198. .2689)
/gene="Z5334"
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/gene="Z5334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="0-island #156; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMNFEFMPELKWSFGYPGAIIFMILAGLAPYLYFKRKNWL"
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/codon start-
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/note="Residues 1 to 131 of 254 are 95.41
residues 1 to 131 of 161 from Escherichia
                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                              /function="orf; Unknown functi
/note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 1 to 316 of 316 are 100.00 pct identical to residues 1 to 316 of 316 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="transport; Transport of small molecules:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1206
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/db_xref="taxon:83334"
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                                                                                                                                                                                                                                                                                          function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glasner, J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pct identical to coli K-12 Strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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4483. .4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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LNQWILFTTIMLSAIPSAKMSLSAH"
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/note="Residues 1 to 39 of 39 are 100.00 pct identical to
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gil6960250[gb]AAF33440.1] (AF233324) S. typhimurium
magnesium transport protein (CORA) (SP:P31138) [Salmonella
typhimurium Lf2]"
                                                                                                                                                                      /note="Residues 4 to 295 of 295 are 92.12 pct identical to residues 8 to 299 of 300 from Escherichia coli K-12 Strain MG1655: B3819"
                                                                                                                                                                                                                                                                                                        complement(4841.
/gene="rarD"
                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4841.
/gene="rarD"
/product="orf, hypothetical protein"
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/db_xref="GI:12518693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3892. .4278)
/gene="z5337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3892. .4278)
/gene="Z5337"
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STPSTGYQPLILGSIKTKLLSSRLNKFNDFEDSFNGLGISVHDISAOKISLLSFOXYA
LGWSATIHFVAQDHFGLDVTDIKNKTYSKYRFFRIWFFLQRHKDFAFKPFFTNFNTIE
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                                                                                                                                                                                                                                                                                                                                                                                    /note="Z5340"
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/gene="Z5339"
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/db_xref="GI:12518690"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="No significant matches"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MNFEFMPELKWSFGYPGAIIFMILAGLAPYLYFKRKNWL"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/note="No significant matches"
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/gene="Z5335"
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alignment_block:
US-09-466-935-2 x AE005613/rev
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                               TGGCGTCTATTGCCGGGCTTCAGACCGGACTGGCGATTCATATTGTGCTG 10442
                                                                                                                                                                           AGTGTTGAAGTGGGCAGGCGCGGCTTACTTGATTTGGCTGGGAATACAGC
                                                                                                                                                                                                                                                             GTTGGCGTGGGGTTGGGGACGCTATTTTCCCGCTCAGTGATTGCGTTTGA 10392
                                                                                                                                                                                                                                                                                   lyTrpArgGlyVal.GlyThrLeuPheSerArgSerValIIeAlaPheGl 72
yGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="pldA"
/note="25342"
6412. .7281
/gene="pldA"
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/gene-"y191"
/function="orf; Unknown function"
/function="orf; Unknown function"
/note="Residues 1 to 161 of 161 are 100.00 pct identical
to residues 1 to 161 of 161 from Escherichia coli K-12
Strain MG1655: B3820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdakotrogevlialaaypigglapayekliyvpadbilihkvi
Wsefenvvlmsicromsylktilotpokifmlavsaavliggmulleimavunhhleba
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Fafyglyrkkiavbaotchilemmillevaaiylfaladsstshkoonpkslkillla
Agivtypellcttaaarelstigffcyigftlmfllavtfygekpgadkhvtftfi
wvalaifydgrks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="enzyme; Central intermediary metabolism: Phosphorus compounds"
/note="Residues 1 to 289 of 289 are 100.00 pct iden to residues 1 to 289 of 289 from Escherichia coli K Strain MG1655: B3821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="orf, hypothetical protein"
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/db_xref="G1:12518694"
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FAQLAFKNOPMMVGNWAQSILHGGVIASALDVAAGLVCVGSTLTRHETISEDELRQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5780. .6265)
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4.847
97.512
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Percent Identity: 96.517
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
ORGANISM
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LOCUS STYCTMAN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name:
                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10041 GCTCGTTGTTTATGCTGGTGGGAGCGCTGTTAGCATCGGCGARGCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10091 TCTATGGATTAAAGGACCAAAGCAGATGAAGGCGCTGAATAAGATTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10141 GTCGATATTATTGTGATGATCGGTTACGCCACCCTTGCTCAACGGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 aLeuTrpI1eLysGlyProLysGlnMetLysAlaLeuAsnLysI1ePheG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ValAspileileValMetileGlyTyrAlaThrLeuAlaGlnArgileAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 lySerLeuPheMetLeuValGlyAlaLeuLeuAlaSerAlaArgHisAla
      rRNA
                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ba3:STYSTMD1
                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium LT2.
Salmonella typhimurium LT2
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (09-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 96086) Waterston, R.
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AF233324.1 GI:6960215
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Salmonella typhimurium
                                                                                                                                               Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs GLIMMER (Salzberg, S., Delcher, A., Kasif, A. and White, O. (1998) NAR 26,544-548), and GeneMark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,1107-1115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 96086)
Washington University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella.
                                                                                                                                                                                                                                                                           NOTES:
/organism="Salmonella typhimurium
/strain="SGSC1412"
/db_xref="taxon:99287"
/clone="STMD1"
<1. 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Department of Genetics, Washington Usst. Louis, Mo 63110, USA
e-mail: scliftonGwatson.wustl.edu or
jspieth@watson.wustl.edu
                                                                                                                        Location/Qualifiers
                                                                                                            .96086
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                                                                                          LT2"
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Missouri 63108, USA
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                                                                                      coli ilvGMEDA operon
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7048
7048
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6580. .6840
6580. .6840
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* * *	* * 1	* * *	- * 1	· * *	* *	* *	* *	**	* *	* *	* *	* *	* 2	. * *	• *	* * *	* * 1	* * *	* *	* *	* *		**		* *	* NO	ř		2200	Seq	REFERENCE 1	ORGANISM MUS Euka	
of 936 t unknown of 142 t		gap of unknown tength 12653 14116: contig of 1464 bp in length	of 331 k		gap of unknown length 10845 11504: contig of 660 bp in length	gap o 10844: conti	9415 10236: contig of 822 bp in length	gap of unknown length 8443 9414: contig of 972 bp in length	7640 8442: contig of 803 bp in length	7639: conti	gap of unknown length 5968 6763: contig of 796 bp in length	gap of unknown length 5572 5967: contig of 396 bp in length	4779 5571: contig of 793 bp in length	4100 4778: contig of interces length		2700 3686: contig of 987 bp in length	of 397 k	gap of unknown length 1605 2302: contig of 698 bp in length and of unknown length	1001 1604: contig of 604 bp in length	gap of unknown contig of 248 k	preserved. 1 752: contig	e 1	overlap relationships among clones to be deduced. However, it should not be assumed that this clone		contigs. Runs of N are used to separate the reads	* NOTE: This record contains 198 individual * Note: This record contains 198 individual * sequencing reads that have not been assembled into	mmitted (10-0AN-2000) Figuretion sequenting Factify, For other nome Institute, 2800 Mitchell Dirive, Walhout Creek, CA 94598, USA TA 2000 this general version replaced dis6686438	4	Unpublished 2 (bases 1 to 256373) Tokat Copyme Institute	renc	nalia; Eutheria; Rodentia; (bases 1 to 256373)	ota.	AC020870 AC020870.2 GI:6984372 HTG: HTGE_PHASE0. house mouse.

16665

16377

16664:

17632 19242 20454 20560

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33 nHisGlyTyrProAla { } :::	17 rLeuSer : 77509 CCTCGTCGC	1 MetThrLeu 77559 ATGACCTTA	Align seg 1/1 to	alignment_block: US-09-466-935-2 x	<pre>alignment_scores: Quality: Ratio: Percent Similarity:</pre>	* *	* * *	· * *	· * *	. * *	* * *	• • ·	* * ;	+ * *	• *	* * :	* * :	* *	* * * 'U1	• * *	· * *	· * *	* * * Us	+ * * 51	· * ·	* * :	* * :	+ + ;	f * *	+ + ;	* *
•	CProGlySer(CCAGGCTCT(MGLUTTPTTPI 	reverse	« AC020870/r	ty: 795.00 10: 4.789 ty: 95.402	7041 6	6042	5591 6	65367 6	5077 6	64040 6	3594 6	2714 6	2639 6	1763	61085 6	0827	9907	9084 5	8530 5	8320 5	7673 5	6935 5	6359 5	5471 5	4634 5	3366 5	2700 5	51829 5	0849 5	50305 5
G1yG1y	GlyAla GGTGCA	PheAla TTTGCC	of: A	/rev	שי	7560:	67040:	6041:	5590:	5366:	5076:	4039:	3593;	2713:	62638:	51762:	61084:	60826:	9906;	9083;	8529:	8319:	7672:	6934:	6358:	5470:	4633;	3365:	2699:	1828:	50848:
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21118
21656
21819
22680
23580
234384
25613

25612:

24383:

23579:

20559: 21117: 21655: 21818: 22679:

37942
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40793
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445301
46418

44115: 45300:

38682: 39549: 40792: 42585:

46417:

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33431:

31202:

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32688:

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gap of unknown length
1: contig of 1610 bp in length
gap of unknown length
3: contig of 1610 bp in length
gap of unknown length
9: contig of 1212 bp in length
gap of unknown length
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gap of unknown length
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gap of unknown length
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gap of unknown length
1: contig of 561 bp in length
gap of unknown length
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gap of unknown length
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gap of unknown length
1: contig of 103 bp in length
gap of unknown length
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gap of unknown length
1: contig of 1303 bp in length
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34616:

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web site: http://www.jgi.doe.gov **NOTE: This record contains 8 individual **NOTE: This record contains 8 individual **sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely * arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows * overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved. 836: contig of 836 bp in length	REFERENCE 1 (bases 1 to 4833) AUTHORS DOE Joint Genome Institute. TITLE Sequencing of Human Chromosome 5 JOURNAL Unpublished REFERENCE 2 (bases 1 to 4833) AUTHORS DOE Joint Genome Institute. TITLE Direct Submission Direct Submission Direct Submission Direct Submission DIRIAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT Center: Joint Genome Institute Center Code: JGI Web after bitter //www.icid.doe.gov	ICCUS ACCI2157 ACCI22167 VERSION ACCI22167 VERSION ACCI22167 VERSION ACCI22167 ACCI22167 VERSION ACCI22167 AC	77109 TCGGCCTATTGTGTGTGATATTGTGATGATCGCTTACGCC 77060 166 ThrLeuAlaGlnArgIle 171	116 PheValAsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPh 132	77459 CCACGGTTATCGCGGCGCGCGGCGCGCGCGCGCTTCAATTGCTGGGCTTCAGACCGGAC 77410 49 rGlyAspSerTyrCysAlaGlyTrpArgGlyVal.GlyThrLeuPheSer 65
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                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Q
Mammalla; Eutheria; Primates; Q
1 (bases 1 to 170178)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
* NOTE: This record contains 175 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
                                                                                                                                                                                                                Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                      Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 170178)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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AC026742.1 GI:7289992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASEO.
                                                                                                                                                                                            Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                  Inpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA HTG 23-MAR-2000 5 clone CTD-3103E19, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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* 17996 * 18076	* 17763 *	* 17609	* 16955	* 16664	* 16597	* 15975	* 15216 *	* 15037 *	* 14183 *	* 13628	* 12949	÷ 12292	* 11269	* 10451	* 10136 *	* 9200 *	* 9083	* 8055	* 7880 *	* 7566 *	* 6916 *	* 6212 *	* * 5561	* 4876	* 4572	* 4072	* 3486	* 2838	* 2657	* 1957 *	* 1343 *	* * 636		* will be seque * the record is
ס ס	contig of 233 bp in gap of unknown lengt	17762: contig of 154 bp in length	17608: contig of 654 bp in length	16954: contig of 291 bp in length	16663: contig of 67 bp in length	16596: contig of 622 bp in length	15974: contig of 759 bp in length	15215: contig of 179 bp in length	of 854 k	14182: contig of 555 bp in length	of 679 b	12948: contig of 657 bp in length	of 1023	of 818 b	of 315 b	of 936 b	of 117 bp in unknown lengt	ig of 1028 of unknown	of 175 b unknown	7879: contig of 314 bp in length gap of unknown length	of 650 b	of 704 b	of 651 b	of 685 b	4875: contig of 304 bp in length	of 500 b		of 648 b	2837: control of 181 bp in length	of Lig	of Eig	ig of 707 b	635: contig of 635 bp in length gap of unknown length	will be sequenced to completion. In the event that the record is updated, the accession number will he preserved.
* 35601 * 36331	* 35490	* 34745	* 33856	* 33124	* 32507	* 31734	* 31681	* 31511	* 31275	* 30694	* 30238	* 29144	* 28932	* 28762	* 27579	26913	26718	26072	25795	24821	24451	23550	23193	23018	22417	21070	20116	20018	19866	19706	19491	19300	19077	18234 18937
36330: contig of 730 bp in length gap of unknown length 36544: contig of 214 bp in length	gap of contig	gap o	gap of contic	gap of	gap of unknow contig of 617	gap of unknown l contig of 773 bp	of	gap of unknown length 31680: contig of 170 bp in length		gap of contig	gap of unknown contig of 456 k	gap of contig	gap of contig	gap of unknown length 28931; contig of 170 bp in length	gap of unknown length 28761: contig of 1183 bp in length	of 666 b	of 195 k	of 646 k	of	of u	gap of unknown length 24820: contig of 370 bp in length	of H	gap of contig	gap of unknown lengt contig of 175 bp in	<pre>gap of unknown lengtl contig of 601 bp in !</pre>	gap of unknown lengt contig of 1347 bp in	gap of unknown l	<pre>gap of unknown lengt contig of 98 bp in 1</pre>	gap of unknown lengt contig of 152 bp in	unknown lengt of 160 bp in	of 215 bp in	of 191 b	of 223 b	of 703 b unknown of 140 b

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alignment_block:
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                                                                                            20056
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                                                                                                                                                                                                                                             gSerVallleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuI
GCAGCATGGTTCCCGGCTTAC
                      AlaAlaLeuPheProGlnPhe 135
                                                                                         CGAGACGGCTGCCACCTCTTCGCCACGCAGACTAATATCC....
                                                                                                                                      TATTCTGATTGTGGTTGTGCGACGTAATGCCCCCGGCCCGACGCATTGCAA 20057
                                                                                                                                                                                                 leTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIle......
                                                                                                               sSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValP 116
                                                                                                                                                                                                                                                                                                                            rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrTserLeuAsnH 34
                                                         heValAsnLeuThrAsnProLysSerIleValPheLeu.....
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of 856 bp in length
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of 689 bp in length
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of 514 bp in
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of 674 bp in
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of 166 bp in le
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of 717 bp in le
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ACCESSION
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LOCUS AE004104
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Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.I. Dodson, R.J., Hatk, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg, J.F., Eisén, J.A., Nelson, W.C., Clayton, R.A., Gwinn, Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Dr, Rockville,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUN-2000) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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AE004104.1 GI:96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="biotype: El To:
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complement(72. 899)
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                                                                                                                                                                                                                                          similarity; putative"
                                                                                                                                                                                                                                                                                      complement(1014. .2030)
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                                                                                                                                                                                                                                                                                                                                   /gene="VC0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /serotype="01"
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/QLFRELYEAHPELQIGGPSHRWVWQSLMATKQCLQLTRQIKIPMLILQAGEEAIVCN
                                                                                                                                                                                                                                                                note="similar to PID:1449198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Vibrio cholerae"
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/translation="MVRCLWAAECCWLPRTMYTTYVARQPIlnakred
/translation="MVRCLWAAECCWLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:L42023 SP:P45173 PID:1007363 PID:1221482 PID:1205585; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MYGQPLSSYTLRYGLADHLSPNDLPLLPTSLPRQVEKVH" complement(4148. .4618)
/gene="VC0139"
complement(4148. .4618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3976. .4095)
/gene="VC0138"
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2670. .3968
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VMFGYTALAAQLGRYIRSPNIMTRMNKLFGSMFMGCGMLLATAKA"
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GLQIGLACHIVLVGIGIGALVAQSALAFTLIKWIGAAYLVWLGIQKWRDRAPLTATTT
                                                                                                                                                                                                                                                                complement(4788. .5117)
/gene="VC0140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="VC0138"
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/note="identified by Glimmer2; putative"
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/db_xref="GI:9654537"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="AAF93315.1"
/db_xref="GI:9654539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKADWQGVEQHCLELGFDLEDVRQELIEAQRWSQDINRLI"
                         KQAIDIPHPLPGQDDQEFWIYVQKGRLGPKREFQVGIHYYHALNPGDKGVLTYQGQRF
                                                                                    /product="conserved hypothetical protein"
/protein_id="AAF93317.1"
/db_xref="GI:9654541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="DPS family protein"
/protein_id="AAF93316.1"
/db_xref="GI:9654540"
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                                                        translation="MPFTLLISLALLIIAAVWFFSHFYRRHMQGENAPQRSAEVTILD/
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                                                                                                                                                                                                                                       alignment_block:
US-09-466-935-2 x AE004104
                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34
                                                              ATGGATATCCATGTTTGGCTTGCCTATCTACTGACCGCGGTGGTGTTTAG
                                                                                             MetThrLeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17
                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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5156. .5260
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6193. .6450
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5322. .5690
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5322. .5690
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/db_xref="G1:9654543"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VC0145"
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EQHSHATPEVIFISIGLAVSMFAHGLRLNHRYHKASFVLFLVAQLLFSKAFWVQLSGS
MVWWLPALLVAASIVAFFLLLPQIDTLIFPVTIMGLMLVQMTWAAGELMLQEATVASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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/db_xref="GI:9654545"
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6567. .7196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFLSFICFYIFKNGSYFSFICLVGCFQFFDFFVVVFIGFLFLFC
SFGLVDFSFFYFVLIVFHLFGVDLLSWFGWWQVFLFCNFIE"
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/db_xref="GI:654542"
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2.855
78.641
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/transl_table=11
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/gene="VC0141"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7245. .7511)
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/note="identified by Glimmer2; putative"
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/note="identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VC0145"
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Gaps:
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Hagrow, M., Carberr, R.L., Goltry, L., Tolertino, E., Hackbrook, R.R., Kas, A., Larbig, K., Lim, R.N., Smith, K.N., Spancer, D.H., Wong, G.K., S., Wulz., Paulsen, L.T., Smith, K.N., Spancer, D.H., Wong, G.K., S., Wulz., Paulsen, L.T., Reizer, J., Smith, K.N., Hancock, R.R., Kas, A., Larbig, K.T., Reizer, J., Smith, K.N., Him, R.N., Spancer, D.H., Hancock, R.R., Kas, A., Larbig, K.T., Lim, R.N., Smith, K.N., Him, R.N., Smith, K.N., Him, R.N., Smith, K.N., Him, R.N., Smith, K.N., Him, R.N., Smith, R.N., R	Complete genome sequence of Pseudomonas aeruginosa PAVI, an opportunistic pathogen JOURNAL Nature 406 (6799), 959-964 (2000) MEDLINE 20437337 REFERENCE 2 (bases 1 to 10475) RUTHORS Stover, C.K., Pham. XQ.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,	ISM Pseudomonas aeruginosa Bacteria; Proteobacteria; gamma subdivision; Pseudomonada Bacteria; Proteobacteria; gamma subdivision; Pseudomonada Pseudomonas 1 (bases i to 10475) 25 1 (bases i to 10475) Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warre RS Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warre RS Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warre RS Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warre Hickey, M.J., Brinkman, F.S., Hufnagde, W.D., Kowalik, D.J., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S. Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Smith, K., Spencer, D., Wong, G.K., Wu, Z., and Paulsen, I.T., Smith, K., Spencer, D., Wong, G.K., Wu, Z., and Paulsen, I.T.,	me: gk cument TION ION N	CGGCACTGGCTGCGCAGCTAGGTCGCTATATTCGTTCACCTAACATAATG LysAlaLeuAsnLysIlePheGlySerLeuPheMetLeuValGlyAlaLe ::: ::: ACCAGAATGAATAACTGTTTGGTTCGATGTTATGGGCTGCGGAATGCT ULeuAlaSerAlaArg 203 ::: ::: GTTGGCTACCGCCAAA 2716	115 alphevalasnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeu 131 ::::::	: ::: ::::: :::: ::::
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                                                                                                                                                                                                                                                                                                                                                                      /product="probable ATP-binding component of transporter"
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GLQIGLALQIAIVAAGVGALLATSALAFSLIKWFGVAYLVYLAVRQWQAPPQALSTDG
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                                                                                                                                                                   AQALMCPSDLLLLDEPTNHLDLDAILWLEEWLKGYPGTLVLISHDRDFLDAVVDHVVH
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CTGCTGGCGCAATACCTGATCATGGGCGCGCACCATGATCGTCGTCGACCT 4836
                                                          GlnLeuMetGlnTyrTleValLeuGlyValThrThrTleValValAspIl 158
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US-09-466-935-2 x AE004937/rev
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::|||:::
TGATCTTCATGCTCGCGGTGCTGCCGCAGTTCATCGACCCGCACCAGCCG
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                                                                                                                                               ...CCACAGGCCTTGAGCACCGATGGCGAACGGCCTCTGGGGGCGACCGTT
                                                                                                                                                                                 LeuLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGln.... 112
                                                                                                                                                                                                                      ACCTGGTGTACCTGGCGGTGCGCCAGTGGCAGGCGCCG......
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20373 21011 21259 22364 233640 24854 27728 27728 27730 28723 29715 29715 29715 29715 29728 29715 29730 28723 29715 29730 28723 29715 29730 28723 29715 29730 28723 29715 29730 28723 29715 29730 28723 29715 29730 28723 29715 29730 29730 29730 29730 29730 297730 29730 29730 29730 29730 29730 29730 29730 29730 29730 297730 297	** 9545 ** 10281 10976 ** 11743 ** 12179 ** 12888 ** 12888 ** 13608 ** 13912 ** 14820 ** 15572 ** 16609 ** 16852 ** 1873 ** 1873
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of 699 bp in length

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gap of unknown length
contig of 1005 bp in length
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contig of 1246 bp in length
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contig of 1000 bp in length
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contig of 671 bp in 1,
gap of unknown length
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contig of 1592 bp in length
gap of unknown length
contig of 504 bp in length
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of 499 bp in le
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alignment_scores:

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Quality:

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Length:

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KEYWORDS
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Percent Similarity:
                                                                                                               AUTHORS
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Submitted (10-JAN-2000) Production Sequencing Facility, Submitted (10-JAN-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA * NOTE: This record contains 69 individual

* sequencing reads that have not been assembled into * sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 62274)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                     2 (bases 1 to 62274)
DOE Joint Genome Institute.
                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                              AC020833.1 GI:6686475
HTG; HTGS_PHASE0.
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Percent Identity: 64.052
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                                                                               DOE Joint
94598, USA
                                                                                   US₽
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	of 719 b	of 568 b	20212: contig of 719 b	* 18716 19493: contig of 777% in length * gap of unknown length	* 17939 18715: contig of 777 being the state of interest length	* 17162 17938: contig of 777 pength gap of unknown length *	* 16427 17161: conflig of 735 b in length * gap of inknown length	* 15739 16426: contig of 688 bp in length * gap of unknown length	15738:	14869: contig of 843 bp in gap of unknown lengt	14026: contig of 148 bp in gap of unknown lengt		13130: contig of 453 b	of 982 b	of 805 b	10890: contig of 618 b	of 594 b	9678:	gap of unl	gap of unknown lengt	gap of unknown lengt 8253: contig of 687 be in	<pre>* 6854 7566: contig of 713 bp in length</pre>	unknown lengt of 399 bp in			* 4767 5296: contig of 530 bp in length	of 1121	of 692 b	of 533 h	of 608 k		1049: contig of 753 b gap of unknown	296: contig gap of	* be preserved.	* will be sequenced to completion. In the event that * the record is updated, the accession number will	* overlap relationships among clones to be deduced. * However, it should not be assumed that this clone	* arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows
FEATURES source				-																	-						-								-		
59221 Loca 1	n (0)	# * 5000	73770	* 49872	* 48116	* 47109	456/5	* * :	* *	* 43259	* 42388	* *	* 39841	* * :	39149	* 37014	+ * ·	* *	* 34311	* 33043	* 32934	* 32153	* 31515 *	* 30781 *	* 29992 *	* 29003 *	* 28058 *	* 27153 *	* 26269	* 178C7	* *	* * * * * * * * * * * * * * * * * * * *	* *	* 23944	* 22941	* 22379	* 21571 *
62274: contig tion/Qualifier: 62274	gap of	gap of	gap of	contig gap of	contig gap of	contig gap of	: contig gap of	gap of	gap of	gap of	43258: contig (gap of	39840: contig gap of a	gap of	gap of		gap of	gap of	gap of	gap of 34310: contig					of Of		29002: contig	28057: contig	contig gap of	b2b8: contig	gap of	gap of	gap of	gap of 24650: contig	23943: contig	22940: contig	22378: contig
	in ngth	length	bp in length	of 1790 bp in length unknown length	of 1756 bp in length unknown length	bp in length	of 1434 bp in length unknown length	igth n	length	nown lengt	of 871 bp in length	known length	in I	unknown length	known lengt	bp in length	known lengtl	known lengt	known	engt in	. ₾ .		of 638 bp in length unknown length			U	of 945 bp in length unknown length	of 905 bp in length unknown length	of 884 bp in length unknown length	or 448 bp in length unknown length	unknown length	unknown length	'⊏.	unknown length of 707 bp in length	of 1003	of 562 b	of 808 bp in

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BASE COUNT
ORIGIN
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LOCUS
                  REFERENCE
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 AUTHORS
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                                                                     TITLE
                                                                                                                                                         AUTHORS
                                    JOURNAL
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Ratio:
                               Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti DNA Res. 7, 331-338 (2000)
                                                                                  Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto, Watanabe,A., Idesawa,K., Ishikawa,K., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.
                                                                                                                                                                                                                                                                                               sequence.
AP003001 BA000012
                                                                                                                                                                                                                           Mesorhizobium loti
                                                                                                                                                                                                                                                                HTG
                                                                                                                                                                                                                                                                              AP003001.1 GI:11994976
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Kaneko, T.
                                                                                                                                                                                        Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                            Mesorhizobium loti (strain:MAFF303099) DNA.
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                  (bases 1 to 345783)
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3.039
67.939
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/clone="RG-MBAC_40H2"
13547 c 13251 g 18170 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-3935
Fax:81-438-52-3934)
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-DB=N_Geneseq_0401 -QFMT=fastap -SUFEIX=rng -GAPOP=12.000
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) DAT: A48443
) DAT: A52691
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/ DAT: V27579
/ DAT: V27578
/ DAT: V24288
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                                     alignment_scores:
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                                                                                                                                  This is the DNA sequence the novel rhtB gene of Escherichia coli (X K-12. The rhtB gene maps at 86 min on the E. coli chromosome. The gene participates in resistance to homoserine. Amplification of the gene results in an improvement of the amino acid productivity of E. coli. The invention provides: the RhtB protein (see Y79298); DNA encoding the RhtB, especially nucleotides 557-1171 of the present sequence; a bacterium, especially of the genus Escherichia, in which L-homoserine resistance is enhanced by amplifying the copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an amino acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of L-homoserine, L-alanine, L-isoleucine, L-valine or
                                                                                       Sequence 1200
                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 10-11;
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Quality: 1061.00 Ratio: 5.176

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/note= "a DNA sequence corresponding to
region (minus the stop codon) is
specifically claimed in Claim 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the L-homoserine resistance gene, rhtB, from Escherichia coli. This sequence may be used to impart L-homoserine resistance on E. coli bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
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                             Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                    (AJIN ) AJINOMOTO CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrLe
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                                                                                                                      2000-414802/36.
DB; B01787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52689
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                                                                                                                                                                                                                                 Zakataeva NP,
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99RU-0104431
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/product= "Yeas"
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                                                                                                                                                                                                                           Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d production;
                                                                                                                                                                                                                              Aleshin VV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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alignment_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-466-935-2 x A52689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the yeas gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, whistidine, isolaucine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                             389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 19-20; 29pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euAsnHisGlyTyrProAlaGly...GlyValTyrCysTrpAlaSerAsp
::::: |||||| |||::: ||||||:::
                                                                                                                                                                                               ProGlnLeu...MetGlnTyrIleValLeuGlyValThrThrIleValVa
                                                                                                                                                                                                                                           CCATTTTGTTCTATGTGTCGTTTTTCGTACAGTTTATCGATGTTAATGCC
                                                                                                                                                                                                                                                                                  erileValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln 140
                                                                                                                                                                                                                                                                                                                   CGGTGCTATTTTTAAACGCGCGTTAATTTTGAGCCTGACTAATCCGAAAG
                                                                                                                                                                                                                                                                                                                                                                 s....LeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAla 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAATTAAGACCACCCCGATATTATTCAACATTGTACGTTATCTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGGGCCAAATACCCTGTTTGTACTCAAAAATAGCGTCAGTAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rProGlySerGlyAlaIle......AsnThrMetThrThrSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSe
AGTACATACGTACCAAAAAGAAACTGGCTAAAGTTGGCAACTCACTGATT
                                                                                                                   laspileileValMetileGlyTyralaThrLeuAlaGlnArgIleAlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                          ....CTGAAGGGTAAAAATAGCGAGGCCAAATCCGATGAGCCCCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTTTATTTGCTCTATCTGGGGAGTAAAATTCTTTACGCGACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...ATTGGCGATGCGGTATTGATGTTTCTGGCATGGGCTGGAGTGGCGAC
                                  euTrpIleLysGlyProLysGlnMet...LysAlaLeuAsnLysIlePhe
                                                                                GAGTTTCTGCTATTTGAGCTTCCTGATTATATCTGGTGCTTTTGTCACGC
                                                                                                                                                               CCACATACGGGAATTTCATTCTTATTCTGGCGGCGACGCTGGAACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         IleAspLeuLys.....SerLeuAlaSerThrGlnSerArgArgHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rLeuPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgThrGlyAspSerTyrCys.....AlaGlyTrpArgGlyValGlyTh
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1.387
66.197
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Gaps:
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10
28.638
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GlySerLeuPheMetLeuValGlyAlaLeuLeuAlaSer

GGTTTGATGTTCGTGGGTTTCGCTGCCCGACTGGCGACG

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alignment_scores:
    Quality:
    Ratio:
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US-09-466-935-2 x T06767
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ID T06767 standard; DNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:T06767
                                                                                            Align seg 1/1 to: T06767
                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                   The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colvelliana melA gene (T06766), and was designated mlgA (mel-linked gene). The role of the encoded protein (R87577) was unclear as deletion subcloning in E. coli demonstrated that only melA was require
                                                                                                                                                                                                                                                                                                                                                                                              Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing \mathbf{l}_\ell oyster settlement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                                                              Sequence 720 BP; 180 A; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuqua WC, Weiner RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5474933-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shewanella colwelliana strain LSTDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mlgA gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mel-linked mlgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T06767;
                                       122 TTTTTACCGACCTTTTTTTCGTCTCAATTACACCAGGTATGTGTATGAC 171
                                                                                                                                                                                                                                                                                                                                                                    Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R87527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-039515/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pigmentation; melanin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marine melA; selectable marker;
                                                                                                                                                                                                                                                                       tor melanogenesis.
25 eAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValT 42
• :::;||||| ::::::: |||
                                                                TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0148945.
90US-0496804.
92US-0974837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-0496804.
                                                                                                                                                            184.00
1.546
56.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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154..159
                                                                                            from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e marker; oyster larva settlement;
p-hydroxyphenylpyruvate-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                            Percent Identity: 27.619
                                                                                                                                                                                                                                              c;
                                                                                                                                                                                                                                           165 G; 210 T; 0 other;
                                                                                          to: 720
                                                                                                                                                                                                                                                                                                                                                                                                                larval
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:V08533
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 07-JUN-1995;
                              07-JUN-1995;
                                                                 08-DEC-1998
                                                                                                 US5846531-A
                                                                                                                                                                                                   Shewanella colwelliana.
                                                                                                                                                                                                                                  MlgA; marine bacterium; melanin synthesis; marine exopolysaccharide;
UV blocker; sunscreen; MelA; ss.
                                                                                                                                                                                                                                                                                   colwelliana MlgA coding sequence
                                                                                                                                                                                                                                                                                                                     11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                      V08533 standard; DNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 AATGGGTCGGTGGGCTCTATCTTGGTTACATCGGCATTAGCATGTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GGGTGTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 AlaAlaGlyAlaIle...AspLeuLysSerLeuAlaSerThrGlnSerAr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 GlyValGlyThrLeuPheSerArgSerValIleAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAATGATCTGTGTTGGCTTATGGTTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuPheMetLeuValGlyAlaLeuLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAs 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGAGCGCTAATAACTCAAGGCTTTGTCACCGCAATTGCTAATCCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCTTCAGCATGCTTATGCGAGCGG.CGGAAAACCCTTAAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAAAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATCAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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   C74446 to C77606 encode the proteins given in B40237 to B43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary
                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
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alignment_block:
US-09-466-935-2 x A52688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the yahN gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                134
                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 672 BP; 130 A; 154 C; 178 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 17-18;
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09-MAR-1999;
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amino acid excretion protein; ds.
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rLeuPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyA
                                         GCGCTGGGCGATGCATTTTATTCCGGGTTGGGTTTGTTTTGGTCTTGCAAC
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                                                                                                                        erLeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAsp
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                                                                 ArgThrGlyAspSerTyrCysAlaGlyTrpArg.....GlyValGlyTh
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  Increased production of L-amino acids by
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ino acid excretion protein; ds.
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GCGCTTATCTCTTATGGTTTGCGTGGTGCAGCATGCGCCGGCCAGTCAACA 330
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    Escherichia bacterium
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                                                                              Troshin
                                                                                                                                                                                                                                                                                                                                                 gene;
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Quality: Ratio: Percent Similarity: Align seg 1/1 to: A52690 US-09-466-935-2 x A52690 129 324 239 189 139 109 494 ATCTGTTTCAGCGATTGTTTCGCCAGTATGGTCGCCAGTTAAATATCGTG 179 ysGlnMetLysAlaLeuAsnLysIlePheGlySerLeuPheMetLeuVal 421 TGGGTAGTT...GGCGTCAGCGTT.....TTGCTGGCGATGAT 280 CCAACAAAGGAAGAC.....GGACTTCAGGCAAAACCAATCAGCTTTTG 96 79 65 58 72 41 alTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrp 57 24 alleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyV 41 22 GCTTTTTGGACTTACACCCTGATTACCGCTATGACGCCCAGGACCGAACAA 71 nArgAlaValPheValAsnLeuThrAsnProLysSerIleValPheLeuA 129 AGTCTGGGATTTTTGATTGTGATGTTACTGTGTGCGGGCATTTCATTTTC TATTCTCGCCCTTAGCTCTGCTACGTCGCATGGATTT....... eGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpIleLysGlyProL TyrIleValLeuGlyValThrThrIleValValAspIleIleValMetIl 162 TTACGGCACTGTCGACGTTTGTTCTGCCG...CAAACACAGGCGTTAAGC laAlaLeuPheProGlnPheIleMetProGlnGlnProGlnLeuMetGln GGCCAGCTTTGCTTTGCAGTTTGTGAACGTCAAAATCATTTTGTACGGTG CGGCATATATTGTCTGGCTGGCG.....TGGAAAATCGCCACCAGC IleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGl 112 laAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAla ACTGGCAGTGATTGACCCGGCAGCGGTACACCTTTTGAGTTGGGCGGGGG rArgSerValIle......AlaPheGluValLeuLysTrpAlaGlyA 79 Arg.....GlyValGlyThrLeuPheSe 54.902 126.00 1.125 from: Percent Identity: \vdash ö 24.510 204 179 493 420 145 279 95 188 65 543 373 323 238

GlyAlaLeuLeu

199

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Seq_documentation_block:
ID A61501 standard; DNA; 1668 BP
XC A61501;
XX A61501;
XX 23-OCT-2000 (first entry)
XX A, vitis hypersensitive response elici
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XW Hypersensitive response elici
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XX Hypersensitive response
XX Agrobacterium vitis.

PN W0200028056-A2.

XX (CORN ) CORNELL RES FOUND INC
XX (CORR                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                           non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences A61501-A61524 represent nucleotide sequences encoding Agrobacterium vitis hypersensitivity response (HR) elicitor proteins (B11630-B11688). The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 82; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC.
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   Quality:
, Ratio:
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                                                                                                                                                                                                                                                                                 for biological control
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Length:
Gaps:
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                                                                                                                                                                                                                                                                                 agents or
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209
                                                                                                                                                                                                                                                                                 polluting
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seq_documentation_block:
ID A61502 standard; DNA;
                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A61502
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US-09-466-935-2 x A61501/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              699 CTGATTGCTTCGATAACCTGGCTGGCGGTTCTCAGCCCCGGCGGATTT
Hypersensitive response elicitor protein; HR; d insecticide; fungicide; antiviral; bactericide;
                                                           A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:11
                                                                                                     23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                           194 LeuValGlyAlaLeuLeuAlaSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 uPheGlnArgAlaValPheValAsnLeuThrAsnProLysSerIleValP 127
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                                                                                                                                                                                                                                                                                               TCGCTGGGGGCCATTCTCTTTACCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                          lyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeuPheMet 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCGCATCCGTTTCGACCTTTTTGTCCAACCCGGCCATTCGAACCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpIleLysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTGATCAGTCTCTACACGCAATTCATCGGCAAGGACACGCCG...CTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyAlaAlaTyrLeuIleTrpLeuGlyIle...GlnGlnTrpArgAlaAla 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCATCCAGCATATTTTCCCCCAATATTCTGGATATCATCAAATTCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rValIle......AlaPheGluValLeuLysTrpAlaG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe
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                       HR; disease resistance;
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    enhancer;
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stress resistance; transgenic plant; ds.

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Sequences A61501-A61524 represent nucleotide sequences encoding CC Agrobacterium vitis hypersensitivity response (HR) elicitor proteins CC (B11630-B11688). The HR is a rapid, localised necrosis that is CC (B11630-B11688). The HR is a rapid, localised necrosis that is CC associated with the active defence of plants against many pathogens, and CC occurs when a pathogenic organism interacts with a nonhost plant (i.e. CC one in which intracellular bacterial growth and disease development do CC not occur). Like other HR elicitors, the A. vitis elicitor functions in CC in walling-off and killing of the pathogen. On grape plants, the A. vitis clictor functions in non-host plants by causing a rapid hypersensitive response that results CC elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor CC proteins, in non-infectious form, are used to treat plants or their seeds CC interest of the control of pathogen resistance and provide control insects, to impart resistance to disease, such as those caused by fund; bacteria CC control insects, to impart resistance to environmental stresses, e.g., CC cold, and to improve nutritional value, e.g., altered oil content. The Same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of CC control of previously untreatable diseases; provide systemic treatment; control of previously untreatable diseases; provide systemic treatment; the next the next form the location control of previously untreatable diseases; provide systemic treatment; control of the control of provious and for the control control of provious and for the control control of the control of the control of the control of the control of t
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Percent Similarity:
1070 CGGCCTCGATGGCCATTGCCTGCTGG.....
                                                                                                                                                                                                                970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1668 BP; 342 A; 462 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burr TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-1998;
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                                                                                                                                                                                                                                            10 LeuLeuThrSerIle.....IleLeuThrLeuSerProGlySerGlyAl 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eliminate the need for biological control agents or polluting
                                                                                                        TGCCATGGTGTCGCGCAATAGTTTTCTTTATGGCCGCAAATCCGGGCTGG
                                                                                                                                                       alleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGly.... 39
                                                                                                                                                                                                             CTGATTGCTTCGATAACCTGGCTGGCCGTTCTCAGCCCCGGCGCGCGATTT 1019
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DB; B11635, B11636, B11637, B11638.
                                               Quality:
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Percent Identity: 20.574
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seq_documentation_block:
ID A48443 standard; DNA; 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1134 GATCATCCAGCATATTTCCCCCAATATTCTGGATATCATCAAATTCGTCG
                                                                                                                                                                                                                                                                                                                            L-threonine resistance; L-threonine synthesis; rhtC; L-homoserine; L-valine; L-leucine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 LeuValGlyAlaLeuLeuAlaSerAla 202
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               Livshits VA,
                                             (AJIN ) AJINOMOTO KK.
                                                                                                              20-DEC-1999;
                                                                                                                                               28-JUN-2000.
                                                                                                                                                                               EP1013765-A1
                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                             E. coli L-threonine resistance gene, rhtC
                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000
                                                                                23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rValIle.....AlaPheGluValLeuLysTrpAlaG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48443
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
               Zakataeva NP,
                                                                                98RU-0123511
                                                                                                              99EP-0125406
                                                                                                                                                                                                                                              Location/Qualifiers 187..807
                                                                                                                                                                                                              /product= "RhtC"
               Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1557
                 Belareva AV,
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                 Tokhmakova IL;
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SXXCCCCCCCCCCCXXX PFFXX DR
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US-09-466-935-2 x A48443
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the L-threonine resistance gene, rhtC, from Escherichia coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 20
P-PSDB;
                                                                                 575
                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                475
                                                                                                                                                                                                                                                                                                                                 431
                                                                                                                                                                                                                                                                                                                                                                                                                  381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 TGGGCATTACCTGCGGCGTA..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 CTCTCAGACCGCTGTCAGTCGTTCCCGTAAAGAAGCGATGATGGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 ATGGTGCACATTGTGGCGCTTATGAGCCCCGGTCCCGATTTCTTTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 840 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 14-15; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIleAsnTh
ACCGCGCGCTGGGCATTTTTGCGCTGATCATTGTCGAAACGCTGGCGTG
                                                                                                                                                             CAGTTTCCTGAAAGGTTTACTGACCAATCTCGCTAATCCGAAAGCGATTA
                                                                                                                                                                                                                                                GAGGCGGTTTCTGCACCTGCGCCACAGGTCGAGCTGGCGAAAAGTGGGCG
                                                                                                                                                                                                                                                                                    LysSerLeuAlaSerThrGlnSerArgArgHisLeu......
                                                                                                                                                                                                                                                                                                                                 TCTGCTGGATGGGTTACCAGATGCTACGT.....GGTGCACTGAAAAAA 474
                                                                                                                                                                                                                                                                                                                                                        euIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAATGGCCTGCCTACACTACGCTGATTATGGTGGGCGGTGGCCTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTGGGCTGGGATTGCCCTGCCTTGGCCTGCATTTGATTATC.....GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyTrpArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...GlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAla 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rMetThrThrSerLeuAsnHisGlyTyrProAlaGly......
                                    LeuMetGlnTyrIleValLeuGlyValThr.......
                                                                                 TCTACTTTGGCTCGGTGTTCTCATTGTTGTCGGTGATAACGTTGGCACT
                                                                                                                       alPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                      uValLeuLysTrp......AlaGlyAlaAlaTyrL 82
                                                                                                                                                                                                 ....PheGlnArgAlaValPheValAsnLeuThrAsnProLysSerIleV 126
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DB; Y99598.
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1.119
49.772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent
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Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.005
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seq_documentation_block:
ID A52691 standard: אמ
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                     The present sequence is the yggA gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A52691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A52691 standard; DNA;
                                                                                                                               Disclosure; Page 24; 29pp; English.
                                                                                                                                                           protein
                                                                                                                                                                      Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid exc
                                                                                                                                                                                                                            WPI; 2000-414802/36
                                                                                                                                                                                                                                                        Tokhmakova
                                                                                                                                                                                                                                                                    Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                     EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli yggA gene
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                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli; yggA gene; amino acid production; excretion protein gene;
nino acid excretion protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....TTTGCCGGGGGGTTATTTGCCGGATTTGGCATTCATTTGATTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnLysIlePheGlySerLeuPheMetLeuValGlyAlaLeuLeuAlaSe
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                                                                                                                                                                                                                 B01789
                                                                                                                                                                                                                                                       IL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                    Zakataeva
                                                                                                                                                                                                                                                                                                                         98RU-0124016.
99RU-0104431.
                                                                                                                                                                                                                                                                                                                                                                  99EP-0125263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                636
                                                                                                                                                                                                                                                                    ΝP,
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                                                                                                                                                                                                                                                                    Nakanishi K,
                                                                                                                                                                                                                                                                     Aleshin
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                                                                                                                                                                                                                                                                     Troshin PV;
                                                                                                                                                                         excretion
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alignment_scores

Sequence 636 BP;

120 A; 143 C; 180 G; 193 T; 0 other;

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seq_documentation_block:
ID T96816 standard; DNA,
XX
AC T96816;
XX
DT 12-MAR-1998 (first &
XX
DX
DA encoding LysG, Ly
XX
XX
KW LysG; LysE; ORF3; LysE
                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:T96816
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: A52691
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                                                                                                                                                                           571
                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                 471
                                                                                                                                                                                                                                                                                                                                    433
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                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
LysG; LysE; ORF3; lysine transport; regulatory protein; export protein;
                          DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                      158 eIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 nArgAlaValPheValAsnLeuThrAsnPro.....LysSerI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 GTCGCCGTGGTTGCTGGCGCTGGTCACCTGGGGCGGCGTAGCCTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 gSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 isGlyTyrProAlaGly...GlyValTyrCysTrpAlaSerAspArgThr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 GCTCGGTCCACAAAATGCTTTTGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                                  GlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAspI1 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTCTTATTACTTTCAAGGTCTTGCACTTGGGGCGGCTATGATCCTACC
                                                                                                                                                                                                                           TGCGCACGGCAAAAGCACAGCGCATTATCAATCTGGTTGTGGGATGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCATGTTGGCAGTGACCTGGCTGAATCCGCATGTTTACCTGGATACTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...TTAGCCAGCGCCGAAGTCATGAAGCAAGGCAGATGGAAAATTATCGC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGTATGGTTTTGGCGCGTTTTAAAACAGCAATGAGCAGTAATATTGAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLys 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCAGTACCACATTATGATTGCCTTACTTTGTGCTATCAGCGATTTGGTC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34
                                                                                                                                                                         ATGTGGTTTATTGCCTTGCAGCTGGCG
                                                                                                                                                                                                   PheMetLeuValGlyAlaLeuLeuAla
                                                                                                                                                                                                                                                  leLysGlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191
                                                                                                                                                                                                                                                                               AAA....ACAATTAGCGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                    TTGTTGTACTGGGCAGCCTTGGCGGCAA.....CTTGATGTGGAACCA 432
                                                                                                                                                                                                                                                                                                                                                                                                             leValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnPro 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....CTGATTTGCGCCGGGATTTTTGGTGGCAGCGCGTTATTGATGCA 19:
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113.00
0.926
58.373
                                                                                                         DNA; 2374
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Gaps: 10
Percent Identity: 24.880
                                                                                                         ВP
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                                                                                                                                                                         597
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                                                                                                                                                                                                                                                                                          CDS
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alignment_scores:
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                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                              US-09-466-935-2 x T96816
                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                  1025 ATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGGCCAGTCTTTTACTGTC
                                                                   1075 CATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.

MB. This sequence has been created from the information given in table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2374 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23 and 26; Page -; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-333867/31
P-PSDB; W37714-16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1995;
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35 lyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAsp 51
                                                                                                                                                                                                      3 LeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSe
                                                                                                                 rProGlySerGlyAlaIleAsnThrMetThrThrSerLeu...AsnHisG
                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95DE-1048222
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1.078
47.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1723..2373)
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= LysE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 A;
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                                                                                                                                                                                                                                                                    from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 C;
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                                                                                                                                                                                                                                                                    2374
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                                                                     1124
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seq_documentation_block:
ID V27579 standard; DNA; 2289 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1423 CGATAAGCAGCGGGTTTGGGTAAAG 1447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1169 TTGTTCATCGCCGGCACCTTGGGCGTTGATCTTTTGTCCAATGCCGCGCC
This nucleotide sequence encodes human hepatocyte nuclear factor 4 isoform alpha 4 (HNF4 alpha 4). Sequences are also provided for
                                                                                  Claim 11; Fig 3; 43pp; English.
                                                                                                                                             Use of hepatocyte nuclear factor 4 - for developing products for diagnosing and determining risk of diabetes and for identifying agents for treatment of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatocyte nuclear factor 4; HNF4 alpha 4; human;
non-insulin-dependent diabetes mellitus; NIDDM; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 heIleMetProGlnGlnProGlnLeuMetGlnTyrIleValLeuGlyVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 nLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPheProGlnP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheValAs 118
                                                                                                                                                                                                                                                                     WPI; 1998-322753/28
                                                                                                                                                                                                                                                                                                                         Krolewski AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9823780-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hepatocyte nuclear factor 4 isoform alpha 4 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V27579;
                                                                                                                                                                                                                                                                                                                                                                             (JOSL-) JOSLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 aGlnArgIleAlaLeuTrpIleLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrLeuAl 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATTGAAGAAACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCGGT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTCATTGCGGTTCTTCTCGTGTGTTTAATTTCTGACGTCTTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGCGGTGGCCACTGACACGCGCAACCGGGTGCGGGTGGAGGTGAGCGT 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lileAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSerVa
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                                                                                                                                                                                                                                                                                                                                                                                DIABETES CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0032043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US21614.
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1291

AATCTTGGCCATGCCGAAGAGCTTGATGAACTGGATCTGCTCGATCATCT 1242

AsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeu.....Ph 132 TCGCTGGGGGACCCTCCCAGCAGCATCTCCTGCAACAGGTT.....GTC

eProGlnPheIleMet.....ProGlnGlnProGlnLeuMetGln. 145

118

1241 GCCACGTGATGCTCTGCAAGGTGGGCAGCAGCAGCAGCAGCTCTCCAAAG 1192

1141 CTGCACCTGGGAACGCAGCCGCTTGATCTTCCCTGGATCGCTCAGCCCCT 1092

160 ValMetIleGlyTyrAlaThrLeu......AlaGlnArgIl 171

CGGCCACGCGAGTCATACTGGCGGTCGTTGATGTAGTCCTCCAAGCTCACTyrIleValLeuGlyValThrThrIleValValAspIleIle 159

1142

1335

101 euAlaSerThrGlnSerArgAisLeuPheGlnArgAlaValPheVal 117 ::|||::: |||:::: |||

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-466-935-2 x V27579/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                            1417
                                                                                                      1387
1385 TATGTTCCTGCATCAGGTGAGGGTGCAGGGGGTGGTGGGGGTGCA 1336
                                                                                                                                                                                                                                                                                                                                                                                                                      1471 CTGTCCCCTGGGTCGGGGCCACTCACATCTGTCCGTTGCTGAGGTGAG 1422
                                                                                                                                                                                                                                                                                                        1421 TGGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes, especially non-insulin-dependent diabetes (NIDDM). Also claimed are: (1) a method for evaluating an agent for use in treating diabetes by evaluating the effect of the agent on an aspect of HNF4 metabolism; (2) the agent identified in (1); (3) a method for treating a cell having an abnormality in structure or metabolism of HNF4, comprising administering the agent to the cell; (4) a method for producing a fragment or analogue of HNF4 polypeptide having wild-type activity; and (5) a method for producing an HNF4 polypeptide or fragment or analogue having a non-wild type activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoforms alpha 1 (see V27577), alpha 2 (see V27578) and gamma (see V27580). HNF4 is a transcription factor whose ligand has not yet been identified. The isoforms of HNF4 are reported to be derived from alternative splicing events. The alpha isoforms have been mapped to chromosome 20 and the gamma isoform to chromosome 8. A claimed method for determining if an animal is at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developing diabetes, comprises evaluating an aspect of HNF4 metabolism or structure in the animal, especially as related to HNF4 from chromosome 20. An abnormality in the aspect of HNF4 metabolism or structure is diagnostic of being at risk for displacements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2289 BP; 489 A; 723 C; 653 G; 424 T; 0 other;
                                                       84
                                                                                                                                                          8
                                                                                                                                                                                                                                                           51 spSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSer 67
                                                                                                                                                                                                                                                                                                                                                                  34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHi
                                                 pLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerL 101
                                                                                           ......CA 1386
                                                                                                                                                        ValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTr
                                                                                                                                                                                                       .....CATTGTGTTGGCAACGATGACGTTGGTTCC.........
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1.043
47.674
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Percent Identity: 22.093
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alignment_scores:
    Quality:
    Ratio:
                                                             alignment_block:
US-09-466-935-2 x X13048/rev
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                                                                                                             Percent Similarity:
                                Align seg 1/1
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:::::::|||:::|||
1091 TGGCATCTGGGTCAAA 1076
                                                                                                                                                                                                                                              A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contide. The computer-based system commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 700-703; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-045171/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
 7 PheAlaTyrLeuLeu....
                                to reverse of: X13048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       faecalis genome contig
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97US-0044031.
97US-0046655.
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                                                                                                          85.00
0.859
41.597
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.....ThrSerIleIleLeuTh 17
                                                                                                                                                                                                         1397
                                                                                                           Percent Identity:
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                                                                                                                                                                                                      1108 G; 2091 T; 13 other;
                                 from: 1
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                                                                                                                            Length:
Gaps:
                                 to: 6590
                                                                                                           238
9
18.908
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	lePheGlySerLeu 191 ::: TTAAAGGTGCCTTG 4541	187 4554
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170 4605	IleValValAspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnAr::::::::::::::::::::::::::::::::::::	154 4654
4655	 AAATTTTGACGCCAATCCACATTGAAATGATTAATCAAACAGGGATGACT	4704
153	Thr	л Л
4705	CTTTACTCTTGCTTTAACCTTSTTGCCAATGGTAATGTTTGGTTTACATC	4754
152	rilevalLenGlvValThr	146
146 4755	GlnGlnProGlnLeuMetGlnTy ::::: ::::::::::::::::::::::::::::::	139 4804
4805	CTATTTTCTTAATCATGCCTGTAGCCGGAGCTATTTCTAATGGC	4848
138	laLeuPheProGlnPheIleMetPro	130
4849	TGATATTATCGTAACGCCAACCATTTCACTTTAGTGATTGGCTTAGCAA	4898
130	aValPheValAsnLeuThrAsnProLysSerTleValPheLeuAlaA	114
114 4899	LeuLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAl	98 4948
4949		4959
97	LeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAsp	81
4960	ATCGGTGTTATTT	4972
81	eSerArgSerVallleAlaPheGluValLeuLysTrpAlaGlyAlaAlaT	64
4973		5008
64	ArgThrGlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPh	48
5009	•	5043
47	CysTrpAlaSerAsp	31
5044		5093
31		17
5094		5143

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/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-444-644-27 + 77.50 114.63 84.57 10785
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-444-644-31 + 77.50 114.63 84.57 10785
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-444-644-32 + 77.50 113.55 93.41 11528
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-444-644-32 + 77.50 113.55 93.41 11528
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-878-801-3 - 76.50 127.96 15.28 2347
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-268-161A-113 + 75.50 127.96 15.28 2347
/cgn2_b/ptodata/2/ina/Sh_COMB.seq:US-08-268-136-1 + 73.00 138.31 25.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 35.211 
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Database sequences: 302621
Database length: 87301344
Search time (sec): 80.320000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-083-741-4 + 7/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-764-233A-1 + 7/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-179-557-16 + 7/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-179-557-16 + 7/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-927-219-130 + 7/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-27 + 7/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-11 + 7/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-476-524-6 + 184.00 379
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-927-219-78 - 82.50 14
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-976-074-4 + 79.50 142
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-Q-/G912_1/USPTO_Spool/US09466935/runat_03052001_075709_12.000
-DB=ISSued_Patents_NA -QPMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.500 -QGAPEXT=7.050 -YGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-TRANS=human40.cdi -LITT=45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=-US09466935_@CGN1_1_59 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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5474933-3
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;Patent No. 5474933
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TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     FILING DATE: 08-NOV-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG........
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FILING DATE: 10-NOV-1992
APPLICATION NUMBER: 496,804
FILING DATE: 21-MAR-1990
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                                                                                                                                                                                                                                                                                                                                            GGGTGTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAA
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                                                                                                                                      gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
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                                      GCTGGGCCTTTATGATGTCGCTGCTCCCCCCTTTTATCAGCGTTGACCAA
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                                                                          \verb|erIleValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln|
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alignment_block:
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US-08-476-254-6
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 Align seg 1/1
                                   US-09-466-935-2 x US-08-476-254-6
                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08476254 Patent No. 5846531
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APPLICANT: WEINER, RONALD M.
APPLICANT: FUQUA, WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202 628-8034
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                       Quality:
Ratio:
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to: US-08-476-254-6
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                                                                                    Percent Identity:
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from:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                             Sequence 78, Patent No. 6
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                      APPLICANT:
                                                                                                   APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
                                                            CORRESPONDENCE ADDRESS
                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TTTTTACCGACCTTTTTTTCGTCTCAATTACACCAGGTATGTGTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG
STREET:
CITY: H
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                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAAAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATCAGTAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaAlaGlyAlaIle...AspLeuLysSerLeuAlaSerThrGlnSerAr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTAAGTCGAGGCGATAACATCAAGTGGATGAACCGCATAGCAGGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCTTCAGCATGCTTGCTTATGCGAGCGG.CGGAAAACCCTTAAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGAGCGCTAATAACTCAAGGCTTTGTCACCGCAATTGCTAATCCAAAAG
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                                                                                                                                                                                                                                                                                                                                               8, Application US/08927219
6187533
                  P.O. Box 4433
                                                                                                                                                                                      Kaisaki, Pamela J.
Furuta, Hiroto
Horikawa, Yukio
                                                                                                                                                                                                                                                       Yamagata, Kazuya
Oda, Naohisha
                                                                                                                                                                                                                                                                                                Bell, Graeme I.
                                        Arnold, White & Durkee
                                                                                   147
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STATE: Texas

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alignment_block: us-09-466-935-2 \times us-08-927-219-78/rev
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; LOCATION:
US-08-927-219-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 78:
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FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 02-OCT-1996
                                                                                                                                                  1186
                                                                                                                                                                                                                          1216
 1134
                                                                         1184 TATGTTCCTGCATCAGGTGAGGGTGCAGGGGGTGGTGGGGGTGCA 1135
                                                                                                                                                                                                                                                                                                 1220 TGGG.....
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/029,679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1441 base pair
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                                    101
                                                                                                              84
                                                                                                                                                                                     89
                                                                                                                                                                                                                                                          51 spSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSer 67
                                                                                                                                                                                                                                                                                                                                    34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
                                                                                                                                                                                                                                                                                                                                                                                                             18 LeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHi 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wilson, Mark B. REGISTRATION NUMBER: 37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U: 77210
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                                                                                                                                                                                 ValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTr 84
TCGCTGGGGGACCCTCCCAGCAGCATCTCCTGCAACAGGTT.....GTC 1091
                                euAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheVal 117
                                                                                                      pLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerL 101
                                                                                                                                                                                                                      Quality:
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1.019
47.093
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                                                                                                                                                                                                                                                                                         Length:
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-976-074-4
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                                                         alignment_scores:
                                                                                                                     US-08-976-074-4
Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                      STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RUSHMORE, THOMAS H.
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA Encoding Prostaglandin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 CTGCACCTGGGAACGCAGCCGCTTGATCTTCCCTGGATCGCTCAGCCCCT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 ValMetIleGlyTyrAlaThrLeu.....AlaGlnArgIl 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990 CGGCCACGCGAGTCATACTGGCGGTCGTTGATGTAGTCCTCCAAGCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCATCTGGGTCAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....TyrIleValLeuGlyValThrThrIleValValAspIleIle 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application US/08976074 5840847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EE: J. Mark Hand - Merck & Co., P.O. Box 2000 - 126 E. Lincoln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METTERS, KATHLEEN NGUYEN, TRUYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRYGORCZYK, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABRAMOVITZ, MARK
                                                                                                                                                             linear
                                                                                                                                                                               single
79.50
0.710
53.081
    Percent Identity:
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                  Length:
Gaps:
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Avenue
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22.275
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seq_documentation_block:
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US-09-466-935-2 x US-08-976-074-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-976-074-4 from: 1 to:
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08083741 Patent No. 5869281
                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: ABRAMOVITZ, MARK

APPLICANT: GRYGORCZYK, RICHAR

APPLICANT: METTERS, KATHLEEN

APPLICANT: NGUYEN, TRUYEN
CORRESPONDENCE ADDRESS: ADDRESSEE: John W. W
                                                          APPLICANT: RUSHMORE, THOMAS H. APPLICANT: SLIPETZ, DEBORAH TITLE OF INVENTION: DNA Encoding NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 tLeuValGlyAlaLeuLeuAlaSerAlaArg 203 :|||:::||| |||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 ATAAAGAA.....TGGATCCGCTTT...GACCAATCAAATGTC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 TCCAAGGCATCGTTTCTGCTTTTTGGCCAGCGGCCTTGGTAATCACTGATTT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 eGlnArgAlaValPheValAsn.....LeuThrAsnProLysSerI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 TCGCCATTCTCATGAAGGCATATCAGAGATTT.....AGACAGAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 leValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnPro 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 TTTTTCAGTAATCTTCATGACAGTGGGAATCTTGTCAAACAGCCTTGCCA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 CCACAACAATGTCCATGAACAATTCCAAACAGCTAGTGTCTCCTGCAGCT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 GAGAGGGAGATGACTTGAGTGG......TTGGCTTTTATCT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 CTGGCGGCCTGGGATGACAAGATGTCTGGACTGCAATCCTGCACAGTTTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 GAGCGGCTCCGTCTTCTGC.....TCCTCAGAGAGCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 lyIle......GlnGlnTrpArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 oAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAla 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCTAGGCAGTGTGATGGCCATTGAGCGG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTGCAGTATTTTTGGTATCTGCATGGTGTTTTCTGGTCTGTGCCCACT 605
W. Wallen,
                                                                                                                                                                                                                                      RICHARD
                                                                                  Prostaglandin
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alignment_block:
US-09-466-935-2 x US-08-083-741-4
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; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-083-741-4
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (908)594-4720 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/083,741
FILING DATE: 25-JUN-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W.
REGISTRATION NUMBER: 35,403
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                  195 GAGAGGGAGATGACTTGAGTGG.......TTGGCTTTTATCT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 CTGGCGGCCTGGGATGACAAGATGTCTGGACTGCAATCCTGCACAGTTTT 194
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                   69 eAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ysAlaGly.TrpArgGly...ValGlyThrLeuPheSerArgSerValI1 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 oAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrC
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ZIP: 070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P. O. Box CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1437 base pairs
                                                                                                                                                                                                                         AlaTleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLeuPh 111
                                                                                                                                                                                                                                                                                                              lyIle......GinGlnTrpArgAlaAlaGly 94
TCGCCATTCTCATGAAGGCATATCAGAGATTT.....AGACAGAAG 420
                                          leValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnPro 141
                                                                                       TTTTTCAGTAATCTTCATGACAGTGGGAATCTTGTCAAACAGCCTTGCCA
                                                                                                                   eGlnArgAlaValPheValAsn.....LeuThrAsnProLysSerI 125
                                                                                                                                                                                 GCGCTTCTTCAAACACAACCTGCCAGACGGAAAACCGGCTTTCCGTATT
                                                                                                                                                                                                                                                                        CCACAACAATGTCCATGAACAATTCCAAACAGCTAGTGTCTCCTGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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Percent Identity: 22.275
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OTHER INFORMATION:
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US-08-764-233A-1
alignment_block:
US-09-466-935-2 x US-08-764-233A-1
                                                                                                   alignment_scores:
                                                   Percent Similarity:
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FEATURE:
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NAME/KEY: misc_feature
LOCATION: 383..760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 927..19874
OTHER INFORMATION: /prod
OTHER INFORMATION: /note
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NAME/KEY:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 30881..35446 OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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OTHER INFORMATION: /product= "module 3 of SorA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 46851..47891
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                                                                                     Quality:
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19870..24556
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13455..19616
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19871..46318
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40190 .46318
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24638..30820
                                                     79.50
1.445
53.398
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/note= "Gene product is highly homologous to type I PKSs are known to be involved in the synthesis of polyketide compounds."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "SorR"
/note= "This gene encodes a protein that is highly homolog the reductase domains of type I PKSs such as eryA from Sancharopolyspora erythraea."
                                                                                                                                                                     /product= "SorM"
note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product=
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                                                         Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Module 1 of SorA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Module
                                                                                                                                                                                                                                                                                                                 "Module 5 of SorB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Module 1 of SorB"
                                                                                                                                                                                                                                                                                                                                                                                   "Module 4 of
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                                                          32.039
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Align seg 1/1

to: US-08-764-233A-1

from: 1

to: 49377

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08179557 Patent No. 5837509
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0
FILING DATE: 01-SEP-1993
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1579/92
FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VRANG, ASTRICTUTLE OF INVENTION: ReconTITLE OF INVENTION: ContaTITLE OF INVENTION: Same
ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MADSEN, Soeren Michael
APPLICANT: JOHANSEN, Eric
APPLICANT: NILSSON, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/UN FILING DATE: 07-JAN-1994
                                         FILING DATE:
                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGACATGGACGCGTTCTACGATCGCGATCCTCGCCTCTCTCGGCGACGTG 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spSerTyrCysAlaGlyTrpArgGly......ValGly 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCATCGATGACGTCGATCGCTTCGACGCGATGTTCTTCGGCATCTCTC 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaG1 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCCTATCCGGCGGCGTGGATGCGGTCACCGAGGTGCCCGCTGGCCGGT 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHisGlyTy 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                  03-JAN-1994
                                         25-MAR-1993
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                                                                                                                        PCT/DK94/00004
                                                                                                                                                                                   DK 0988/93
                                                           US 08/036,681
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; TOPOLOGY: US-08-179-557-16
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US-09-466-935-2 x US-08-179-557-16
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    Quality:
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Percent Similarity:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 30307/140/PLVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
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                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GlyAspSerTyrCysAla.....GlyTrpArgGlyValGlyThrLeuPh 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 snHisGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThr 49
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TTGTTCCAACACAAGCAACAGCACCAATTTTGATTATCGTTGGGATGATG 770
                                                                                      AACAGCAATTATGTTTGCTATCTCAAGCTTGTTCTTACCACTTCTTGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                             GCGACAGGAATCTTTACTGATGAAGATTTGAAAGACATGGAAACAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaGlyAlaIle......AspLeuLysSerLeuAlaSerThrGl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAACAACCTTTGGTGCAGCATTTGGTCCAAAAGGATTTGGTTCTTTATT
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                                      euGlyValThrThrIleValValAspIleIleValMetIleGlyTyrAla
                                                                                                                          eProGlnPheIleMetProGlnGlnProGlnLeuMetGlnTyrIleValL 149
                                                                                                                                                                        TCTGCTGCCGGAATCGGTGCAGGAGGACGTACTGGTCTTGCATCAGTTGT 670
                                                                                                                                                                                                                                                       CTCCAATCGGAGCAATTTTCGGAACATCAAATACAACCGTTTATGTTGAG
                                                                                                                                                                                                                                                                                                                                              TGGTTTCTCATCAAAAATGGACAAAGCTTTGTTTGCTGACATGATTGCTA
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                                                                                                                                                                                                     .....LeuAlaAlaLeuPh 132
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49.561
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Align seg 1/1 to: US-08-927-219-130

from: 1

to: 10014

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seq_documentation_block:
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                                                                                                                                                                      ; STRANDEDNESS: ; TOPOLOGY: lii
US-08-927-219-130
alignment_block:
US-09-466-935-2 x US-08-927-219-130
                                                                                                                alignment_scores:
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                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: ARCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 sAlaLeuAsnLysIlePheGlySerLeuPheMet 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60 FILING DATE: 02-OCT-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                LENGTH:
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                                                                                            Quality:
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                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                             512/474-7577
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Furuta, Hiroto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikawa, Yukio
                                                                                                                                                                                            linear
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                                                      78.00
0.867
46.392
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                                                        Gaps:
Percent Identity:
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-27
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08444644 Patent No. 6015555
                                                                                                                                                                                                                                                                    GENERAL INFORMATION: Phillip M.
APPLICANT: Friden; Phillip M.
TITLE OF INVENTION: TRANSFERR
TITLE OF INVENTION: CONJUGATE
TITLE OF INVENTION: CONJUGATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5695 CAAGGACAGAGTCAGCG..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5958 GGAGCCACCAAGAGATCCATGGTGTTCAAGGACGTGCTGCTCCTAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 PheGlnArgAlaValPheValAsnLeuThrAsnProLysSerIleValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 GlyValThr.....ThrIleValValAspIleIleValMetIleGlyTy 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 euMetGln......TyrIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 eLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln...ProGlnL 143
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS.
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 rAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 lyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 spargThrGlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 IleIleLeuThrLeuSerProGlySerGlyAlaIleAsnThrMetThrTh 30
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                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                           STATE: N
COUNTRY:
                                                                                                                                                          CITY:
                                                                                                                                                                             STREET:
                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...AGCACATGTTCTTTCCCCCTTCCAGGTTTCTAGTTTTATGGGTAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aTyrLeuIleTrpLeuGlyIleGlnGlnTrpArg......AlaAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....AAGCTGACTTGCCCAGCGTCACTGAGTTG 5857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ThrLeuAlaGlnArgIleAlaLeuTrp 174
                                                                                           02173
                                                                                                                                                          Lexington
                                                                                                                                     MA
                                                                                                                                                                                    Two Militia Drive
                                                                                                                USA
                                                                                                                                                                                                       Hamilton,
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             TRANSFERRIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                        CONJUGATES
                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                       Brook, Smith & Reynolds, P.C
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nSerArg 107	91 rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGln ::: :::::::::::::::::::::::::::::::::
6445	6445
GlnTrpA 91	74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnG
luValLe 74	58 ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheG ::: :: :: :: 6410 AAGGTTTCAATATTCTTTACTGCCACCGCCATCGCC
AlaGlyTrp 57 GCAGTGTGG 6409	45AlaSerAspArgThrGlyAspSerTyrCysAl :::
CAACGCA 6359	32LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp.
31 CGCCAGG 6309	21 GlySerGlyAlaIleAsnThrMetThrThrSer
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169 9 .444	alignment_scores: Quality: 77.50 Ratio: 0.969 Percent Similarity: 47.337 Percent Identity: 25.
ession	; NAME/KEY: misc_feature ; LOCATION: 110785 ; OTHER INFORMATION: /note= "Function = "Expre ; OTHER INFORMATION: Vector Coding Sequence"" US-08-444-644-27
	E SOURCE: PAH4625
	; MOLECULE TYPE: DNA (genomic)
	: LENGTH: 10785 base pairs : TYPE: nucleic acid : CTPANDEDURES: 40.510
	MATION FOR SEQ ID NO:
	TELEPHONE: (617)
	KET KUM
	TION:
	APPLICATION N FILING DATE:
	: 07-SEP-1990 TION DATA:
	ATION NUMBER: PCT
	APPLICATION NUMBER 11 OF THE PARTY OF THE PA
	TION DATA:
	ATION NUMBER: US
	CLASSIFICATION:
	APPLIC
25	SOFTWARE: PatentIn Release #1.0, Version #1.

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seq_documentation_block:
Sequence 41, Application US/08444644
Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN REGISTRES OF INVENTION: CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-41
                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/232,246
FILING DATE: 07-7UL-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner: Richard w
                                                                                            TELEPHONE: (617) 861-95-
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10844 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                       NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6646 CTGG 6649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02173
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6596 ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGTTAACAG 6645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 uTrp 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Mil:
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLe 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lnProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValVal 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnG
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                                                                                                                 861-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFERRIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/444,644
                                                                                              41:
                                                                                                                                                                                     ALK88-15AAAZ
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alignment_block:
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                                                                        seq_documentation_block:
                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-444-644-41 from: 1 to: 10844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-466-935-2 x US-08-444-644-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                      Sequence 18, Application US/08444644 Patent No. 6015555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8428 AATATACAACCCAACTGAAGCTACCGGACGCGTGACCTGCTGGCAACGCA 8477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8564 ..TGTTTTAGCTCGTCGCTCAGGCGTTCGCTGGCGGCGGCGATCTCCTCT 8611
                                                                                                                                                                       8764 CTGG 8767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genom FRAGMENT TYPE: N-terminal IMMEDIATE SOURCE:
                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG...GITTCAATATTCTTTACTGCCACCGCCATCGCC...... 8563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe 74
                                                                                                                                                                                                                       uTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                           lnProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValVal 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnG 140
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                                                                                                                                                                                                                                                                      ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGCTTAACAG 8763
                                                                                                                                                                                                                                                                                                              AspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLe 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..ArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArg 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTTTATCAAACTTCGCGCTGTATTCCCGCAGGGCCTCATCGCCGCGT. 8686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.50
0.969
47.337
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Vector Coding Sequence""
                                                                                                                                                                                                                                                                                                                                                                .....GCTTTCACGTTATCGAGAATATCGTTA 8713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 25.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GGTAACCGT 8637
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NAME/KEY: misc_feature;
LOCATION: 1.11528
OTHER INFORMATION: /note= "Function="Expression Vector;
OTHER INFORMATION: Coding Sequence" |
US-08-444-644-18
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Quality:
                                                                                                                        alignment_block:
                                                                 Align seg 1/1
                                                                                                        US-09-466-935-2 x US-08-444-644-18
                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Friden, I TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: CITCUL MOLECULE TYPE: DNA
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US O'
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: application number: US 08/232,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: pAH4602
                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                             21 GlySerGlyAlaIleAsnThrMetThrThrSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,480 REFERENCE/DOCKET NUMBER: AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagner,
                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hamilton, Brook, Two Militia Drive
                                                                     to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friden, Phillip M.
VENTION: TRANSFERRIN RECEPTOR SPECIFIC
VENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                                                                                                                                                           NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                     US-08-444-644-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                         77.50
0.969
47.337
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                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALK88-15AAAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith & Reynolds,
                                                                       from: 1
                                                                                                                                                                                              Length:
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0:
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seq_documentation_block:
; Sequence 32, Application US/08444644
; Patent No. 6015555
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Friden, Phillip M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9400 ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGTTAACAG 9449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9249
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/444,644
FILING DATE:
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 lnProGlnLeuMetGlnTyrTleValLeuGlyValThrThrIleValVal 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9214 AAG...GTTTCAATATTCTTTACTGCCACCGCCATCGCC......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9114 AATATACAACCCAACTGAAGCTACCGGACGCGTGACCTGCTGGCAACGCA 9163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLe 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTTCACGTTATCGAGAATATCGTTA
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156	140 lnProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValVal
140 7910	124 SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnG ::::::: :: :::::
123 7861	108ArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLys
107 7835	91 rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArg ::: :::::::
7787	7787
91	74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA
74 7787	58 ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe ::: ::: ::: ::: 7752 AAGGTTTCAATATTCTTTACTGCCACCGCCATCGCC
57 7751	45AlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrp ::: ::: 7702 CGCCTGGCGTTTCTACATCTACCGGCGGAGTTTTTGCGCAGTGTGG
44 7701	32LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp ::: 7652 AATATACAACCCAACTGAAGCTACCGGACGCGTGACCTGCTGGCAACGCA
31 7651	21 GlySerGlyAlaIleAsnThrMetThrThrSer
	Align seg 1/1 to: US-08-444-644-32 from: 1 to: 12127
	alignment_block: US-09-466-935-2 x US-08-444-644-32
	alignment_scores: 77.50 Length: 169 Quality: 77.50 Gaps: 9 Percent Similarity: 47.337 Percent Identity: 25.444
	NAME/KEY: misc_feature; LOCATION: 112127; OTHER INFORMATION: /note= "Function = "Expression; OTHER INFORMATION: Vector Coding Sequence" " US-08-444-644-32
	IMMEDIATE SOURCE: CLONE: pAH4807 FEATURE:
	TELEPHONE: (617) TELEPAX: (617) INFORMATION FOR SEQ
	REFERENCE/DOCKET NUMBER: A TELECOMMUNICATION INFORMATION
	ATTORNEY/AGENT INFORMATI NAME: Wagner, Richard REGISTRATION NUMBER:
	APPI FILI
	; APPLICATION NUMBER: PCT/US90/05077 ; FILING DATE: 07-SEP-1990 ; PRIOR APPLICATION DATA:
	TATOR APPLICATIO

Quality:

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seq_documentation_block:
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; LOCATION: US-08-927-219-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7911
                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7988 CTGG 7991
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-CCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 10-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: AND HNF-4ALPHA
                                                      FEATURE
                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 61 FILING DATE: 02-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                      LENGTH: 844 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                         NAME/KEY:
                                                                       TOPOLOGY:
                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGTTAACAG 7987
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                                                                                                                                                                                                                                                 Wilson, Mark B.
Wilson, Mark B.
Wilson, Mark B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaisaki, Pamela
Furuta, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oda, Naohisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamagata, Kazuya
                                                                                                                                                                                    512/474-7577
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                    429..515
                                                                         linear
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                                                                                                                                                                                                                                                                                                                 10-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                    us 60/028,056
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                                                                                                                                                                   46:
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                                                                                                                                                                                                                                         ARCD: 272
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alignment_scores

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APPLICANT: Negulescu, Paul
APPLICANT: Offermanns, Stefan
APPLICANT: Simon, Melvin
APPLICANT: Zuker, Charles
ITITLE OF INVENTION: PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE
FILE REFERENCE: 08366/002001
CURRENT APPLICATION NUMBER: US/08/878,801
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: US 60/020,234
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-466-935-2 x US-08-927-219-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-878-801-3
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-927-219-46
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08878801 Patent No. 6004808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 ATGTTGCTTACAGTTTCATCAGGCACACAGAAGAGGCCCCAGCACGAAGCA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 CAAGGACAGAGTCAGCG..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GTTTCTTGCCCAAGGACAC.....AGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 GTGCTGCTCCTAGGTGAGGCGGCTGCCTGCCCTGGCCAGGGCTCCAGGGA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 GCGAGCACCTGCTCGGAGCCACCAAGAGATCCATGGTGTTCAAGGAC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 etGlnTyrIleValLeuGlyValThr.....ThrIleValValAspIle 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 eLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGlnLeuM 144
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

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		GlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAs 51 ::: :::::: ::: GTCTCGCCAGCTCCAGGGCTCCAAAGGTGGATTGGCTCCTGCACCTCCAT 132	user.ProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHis 34	TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18 :::::: :::: :::: ::: TGGTGGTGGCAGTGGCTGGTGGTCTCCTGTGTCTTGTCT	gn seg 1/1 to: US-08-453-695A-113 from: 1 to: 2347 5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18	_block: 6-935-2 x US-08-453-695A-113 6-935-2 x US-08-453-695A-113 from: 1 to: 2347 g 1/1 to: US-08-453-695A-113 from: 1 to: 2347 g 1/1 to: US-08-453-695A-113 from: 1 to: 2347 grapheAlaTyrLeuLeuThrSerIleLeuThrLe 18 ::: :::	Guality: 75.50 Quality: 75.50 Ratio: 1.606 A similarity: 61.842 Percent Identity: 32.895 Length: 32.895	ENCE CHARACTERISTICS: WGTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear SCOTES: QUALITY: 75.50 Ratio: 1.606 Rat	ANTON FOR SEQ ID NO: 113: ANTON FOR SEQ ID NO: 113: METH: 2347 base pairs PE: nucleic acid Gaps: CDNA -695A-113 -695A-113 -70 Ratio: 1.606 Ratio: 1.60	LEPHONE: 312/474-6300 LEPAX: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 25-3856 ATION FOR SEQ ID NO: 113: RENCE CHARACTERISTICS: NOTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear 3ULE TYPE: cDNA -695A-113 -505CTCS: Quality: 75.50 Ratio: 1.606 Ratio: 1.607 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Ratio: 1.607 Ratio: 1.606 Ra	PERENCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-6300 LEFAX: 312/474-6300 LEX: 25-3856 ATION FOR SEQ ID NO: 113: ENCE CHARACTERISTICS: MCTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear SULE TYPE: cDNA -695A-113 -SCORES: -SCORES: -SCORES: Quality: 75.50 Ratio: 1.606 Quality: 61.842 Percent Identity: 32.895 -block: -595A-113 -595A-113 -76 -76 -76 -77 -78 -78 -78 -78 -78 -78 -78 -78 -78	REEY AGENT INFORMATION: RE: NO. 5798143 and, Greta E. 3ISTRATION NUMBER: 35,302 FERENCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 312/474-0408 LEFAX: 25-3866 ATION FOR SEQ ID NO: 113: RANDEDNESS: single POLOGY: linear COULE TYPE: CDNA -8050A-113 -8050FES: CDNA -8050A-113 -8050FES: Length: 76 Gaps: Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 -010ck: 6-935-2 x US-08-453-695A-113 6-935-2 x US-08-453-695A-113 from: 1 to: 2347 gl/1 to: US-08-453-695A-113 from: 1 to: 2347 gl/1 to: US-08-453-695A-113 from: 1 to: 2347 gl/1 li:::	ASSIFICATION: 530 RNEY/AGENT INFORMATION: SSISTRATION UNUMBER: 35,302 FERENCE/DOCKET NUMBER: 32658 TOMMUNICATION INFORMATION: LEPAN: 312/474-6300 LEFAX: 312/474-6300 LEFAX: 312/474-6300 LEFAX: 312/474-6300 LEPAX: 312/474-648 LEPAX: 312	ENW APPLICATION DATA: LING DATE: LING DATE: ASSIFICATION: 530 RNEY/AGENT INFORMATION: ME: NO. 5708143 and, Greta E. 315TRATION NUMBER: 35,302 315TRATION NUMBER: 35,302 STSTRATION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 LEX: 25-3856 ANTION FOR SEQ ID NO. 113: RATION FOR SEQ ID NO. 113: SECORES: Single POLOGY: linear COLOGY: linear COLOGY: linear COLOGY: 1.606 RATION FOR SEQ ID NO. 113: COUGHIT!: 61.842 Percent Identity: 32.895 Block: COLOGY: 1.606 RATION FOR SEQ ID NO. 113: COUGHIT!: 1.606 RATION FOR SEQ ID NO. 113: COLOGY: 1.606 CAPPACION FOR SEQ ID NO. 113: COLOGY: 1.606 CAPPACION FOR SEQ ID NO. 113: COLOGY: 1.606 CAPPACION FOR SEQ ID NO. 113: ERATING SYSTEM: PC_DOS/MS-DOS STWARE: Patentin Release #1.0, Version #1.25 ENT APPLICATION DATA: PLICATION NUMBER: US/08/453,695A LING DATE: ASSIFICATION: 530 RNEY/AGENT INFORMATION: MS: NO. 5708143 and, Greta E. 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ALIGNMENTS

A;Cross-references: GB:AE000458; GB:U00096; NID:92367299; PIDN:AAC76827.1; PID:917902 A;Experimental source: strain K-12, substrain MG1655 R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R. Science 257, 771-778, 1992 A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84. A;Reference number: S30660; MUID:92358234 A;Accession: S30714 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A65187 C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: A65187; S30714 밁 QΥ 멍 Qy Qy C;Genetics: A;Gene: yig A; Molecule type: DNA
A; Residues: 'V', 2-138 <DAN>
A; Cross-references: EMBL: M8
A; Note: the nucleotide seque hypothetical 15.4 kD protein in recQ-pldB intergenic region - Escherichia coli (strai N;Alternate_names: hypothetical protein f138 A; Molecule type: DNA A; Residues: 1-138 <BLAT> A; Status: nucleic acid sequence not shown; A;Status: preliminary; nucleic acid sequence not shown; translation not shown Query Match Best Local (Matches 121 188 128 61 Local Similarity FGSLFMLVGALLASARHA 205 LAALFDQFIMDQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALMIKGPKQMKALNKI 187 FGSLFMLVGALLASARHA 138 LAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWIKGPKQMKALNKI 120 137; Conservative EMBL:M87049 64.7%; 99.3%; Score 686; DB 2; Pred. No. 5.7e-58; 1; Mismatches 0; translation ç the Length 138; EMBL Data Library, November Indels not shown 0, Gaps 0; 1992

nypothetical prote

RESULT G82358

conserved hypothetical protein VC0136 [imported] - Vibrio cholerae (group Ol strain

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A; Experimental source: strain PAO1 C; Genetics: A; Gene: PA5249
Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa (;Date: 15-Sep-2000 #text_change 31-16;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-16;Accession: C82990 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
                                            Вb
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                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <STO>
A;Cross-references: GB:AE004937; GB:AE004091; NID:g9951553; PIDN:AAG08634.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
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A; Residues: 1-205 <HEI>
A; Cross-references: GB: AE004104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Accession: G82358
                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome A; Reference number: A8295
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C:Superfamily: hypothetical protein b1798
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                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C82990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PA5249 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                               Matches
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: A82950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                          MLVSTWFAFFLACWAISLSPGAGAIASMSCGLQYGFARG----
                                                                              MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTNPKSIVFLVALFPQFIDPTRDHWPQFLVLGITTVTIDAIVMFGYTALAAQLGRYIRSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIHVWLAYLLTAVVFSLAPGSGTVNSISNGLSYGTRHSLGAIIGLQIGLACHIVLVG-I 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHG--YPAGGVYCWASDRTGDSYCAGWR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 68
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
-GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLAS 103
                                                                                                                                                                                                                                                                                                                                                                                                            sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.3%;
                                                                                                                                               36.7%; Score 389; DB 2; 36.4%; Pred. No. 1.2e-29;
                                                                                                                             37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 459.5;
Pred. No. 2.
                                                                                                                           Mismatches
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                                                                                                                                                                   Length 209;
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Larbig,
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K.; Lim,
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hypothetical protein b1798 - Escherichia coli (strain K-12) C;Speciles: Escherichia coli (strain K-12) C;Speciles: Escherichia coli (strain K-12) C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 29-Sep-1999 C;Accession: F64940 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; RSE, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                             A; Molecule type: DNA
A; Residues: 1-212 <BLAT>
                                                                                          A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617 A;Accession: F64940
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A; Residues: 1-241 <WHI>
A; Cross-references: GB: AE002038;
A; Cross-references: GB: AE002038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
C75329
       A; Experimental source:
                          A; Cross-references: GB: AE000274;
                                                                         A; Status: preliminary; nucleic acid sequence not shown;
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A;Accession: C75329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        174 WIKG-PKQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 IIVMIGYATLAQRIALWIKGPKQMKALNKIFGSLFMLVGALLASARHA 205
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                                                                                                                                                                                                                                                                                                                                                     RLQGNPRFQRGQKVASGGAMIALGTYVAVER 241
                                                                                                                                                                                                                                                                                                                                                                                                                         AMTELLNPKTALFFLAVIPQFVKPATGHVFGQFLLLGTTSVVVNTLNAMLVATLAGFLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                             VFVNLTNPKSIVFLAALFPQFIMPQQPQLM-QYIVLGVTTIVVDIIVMIGYATLAQRIAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR-----G 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDGERPLGRPLTLVLRGFLVNASNPKAVIFMLAVLPQFIDPHQPLLAQYLIMGGTMIVVD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFLVAAVVLALLPGPGLMYILARSLGGGR------WAGIQSALGTGAGGMVHVLASAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIVMAGYTGLAARVLRVLRSPRQQKLVNRTFASLFVGAAGLLATVRRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLQIGLALQIAIVAAGVGALLATSALAFSLIKWFGVAYLVYLAVRQWQAP-----PQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
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strain K-12, substrai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 228; DB 2;
Pred. No. 2.6e-14;
       substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
         NID:g1788089;
in MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
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                          PIDN:AAC74868.1; PID:g17880
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                                                                                                                                                                                    V.; Riley,
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                                                                               shown
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A;Authors: Foolger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueely, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serou akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aththors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: F69975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E., Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Bacillus C; Date: 05-Dec-1997
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                                              δÃ
                                                                                                            В
                                                                                                                                                       Qγ
                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-210 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: F69975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dihydrodipicolinate reductase homolog yrhP - Bacillus subtilis
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     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: Z99117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Genetics:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
     122
                                                   114 AVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 RIALWIKGPKQM-KALNKIFGSLFMLVGALLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                          63 LFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDL-----KSLASTQSR--RHLFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AWAGVATLIKTTPILFNIVRYLGAFYLLYLGSKILYAT----LKGKNSEAKSDEPQYGAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK---SLASTQSRRH--L 110
                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LEWWFAYLLTSIILTLSPGSGAI----NTMTTSLNHGYPAG-GVYCWASDRTGDSYC--A 55
                                                                                                                                                                                                                                                                 8 AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR-----GVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LNYW-TYLVGAIFIVLVPGPNTLFVLKNSVSSGMKGGYLAACGVF-----IGDAVLMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVTQYIRTKKKLAKVGNSLIGLMFVGFAARLAT
     GSLSNILNPKTVLVYVTIMPQFINLNGNINQQLIILASILTLLAVLWFLFLVYIIDYAKK 181
                                                                                                         VIAKSVILFTTIKYLGAAYLIYLGVKSFFAKSMFSLDDMQSQAKNMASSPKRYYKTSFMQ
                                                                                                                                                                                                             AYIPIAAMMVIIPGADTMLVMKNTLRYG-PKAGRYNILGLATGLSF---WTVIAILGLSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKRALILSLTNPKAILFYVSFFVQFIDVNAPHTGISFFILAATLELVSFCYLSFLIISGA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                            18.4%; 27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.4%; 28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GB:AL009126;
168
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                                                                                                                                                                                                                                                                                                                                            Score 195; DB 2; Pred. No. 3e-11;
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Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g2634966; PIDN:CAB14652.1; PID:g2635156
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                                                                                                                                                                                                                                                                                                                       88;
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                                                                                                                                                                                                                                                                                                                    Indels
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Query Match
Best Local Similarity
Matches 57; Conserv
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hypothetical protein BH0429 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 C;Accession: E83703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
  A;Cross-references: GB:AP001508; GB:BA0000004; NID:g10172890; PIDN:BAB04148.1; GSPDB:GA;Experimental source: strain C-125
                                                        A; Molecule type: DNA
A; Residues: 1-207 <STO>
                                                                                                                                           A; Reference number: A; Accession: E83703
                                                                                                                                                                                                                                 R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004864; GB:AE004091; NID:g9950740; PIDN:AAG07895.1; GSPDB:GNA;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A82950; A; Accession: G83082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID: 20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PA4507 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                   A; Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: PA4507
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A; Experimental source:
                                                                                                                A; Status: preliminary
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 NPKALLFCSVLLPQFVSPEAGSLAVQFAALGTVLVLVGLAFDCAYALAGGRLGRWLASRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQRIALWIKG-P 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 WIKGPKOMKALNKIFGSLFMLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAQRLQQWGFGGLLIGFGVRLALLR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAPWTFDLVRLLGAVYLAWLGLQMLRGGGLALPTSDAGSAPVVPHADRRALLRGLLTNLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSVIAFEVLKWAGAAYLIWLGIQQWRAAG-AIDLKSLAST----QSRRHLFQRAVFVNLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFLIALAVVYLVPGPDMLLLFQTGARQGRRAALVTALGLALARACHVLMAA-TGLALLFR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYC--WASDRTGDSYCAGWRGVGTLFS
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58; Conserv
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                                                                                                                                                                         sequence of the alkaliphilic bacterium Bacillus halodurans
50; MUID:20263314
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Pred. No. 4.6e-11;
11; Mismatches 106
                                                                                                                                                                                                                                                            Sasaki, R.;
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                                                                                                                                                                                                                                                            Masui, N.; Fuji,
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A.; Larbig,
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Conservative

18.1%; Score 192.5; 26.3%; Pred. No. 5e-Live 50; Mismatches

DB 2;

Length 207; Indels

23;

6

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conserved hypothetical protein VCA0355 [imported] - Vibrio cholerae (group Ol strain N: C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: C82471
R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                      RESULT
C82471
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                                                                                                                                                                                                                                                                                                                                                                                                                 В
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A; Title: DNA Sequence of both chromosomes A; Reference number: A82035; MUID: 20406833
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A;Accession: G82200
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein VC1421 [imported] - Vibrio cholerae (group O1 c;Species: Vibrio cholerae (c;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Accession: G82200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: VC1421
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-212 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW--- 57
                                                                                                                                                                                                                                                                LSSAKNLLKNASFMRWMEGTTGVVLVALGIKL
                                                                                                                                                                                                                                                                                                                                                                                                              ATFSAIGISAILAQSAELFQIVKMVGAAYLIWLGISSLRSLMKTGQGIEVASLAHAQFRL 113
                                                                                                                                                                                                                                                                                                    AQRIALWIKGPKQMKALNKIFGSLFMLVGALL
                                                                                                                                                                                                                                                                                                                                     TRSLREGFLSNVLNPKTAVFYLAFLPQFINPDYSPLAQSLLMALIHFAIAMVWQCGLAGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVIQNFEAFFIAITILTLTPGLDTALVIRNTSRAGFADG---C---TTSLGICFGLFVH 53
                                                                                                                                                                                                                                                                                                                                                                    HLFQRAVFV-NLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRIA-LWIKGPKQMKALNKIFGSLFMLVGALLASARH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRA----AGAIDLKSLASTQSRR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKVGQLLMRSSFIKNQMHRIKGGLLALIGLQVAFSKN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYKKGIIMNVLNPKVSLFFLALLPQFVNSGAGSAPWQMLLLGVVFLIQAFIIFSLVSWFA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITAAVVGISALIYQSALAFTVVKYAGAAYLLYLAWKAFQEKGEGLSIDKQ---TTLAYGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAG---AIDLKSLASTQSRRH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDLTSLLSFLGVAVLLTLMPGPDILFVLAQSMSQNRQAGIV-----TALGLCTGLLVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 190; DB 2; 27.4%; Pred. No. 8.9e-11; tive 35; Mismatches 99
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             the cholera
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             pathogen
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H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A;Gene: VCA0355
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                                                                                                                                                                                                                                                                              Matches
                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
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A; Status, Front A; Molecule type; DNA
A; Molecule type; DNA
A; Residues: 1-207 <STO>
A; Cross references: GB: AE004786; GB: AE004091;
- """" PAOTIMENTAL SOURCE: Strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: PA3665
C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
A;Accession: D83187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA3665 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004372; GB:AE003853; NID:g9657741; PIDN:AAF96263.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-208 <HEI>
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A;Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 LAQRIALWIKGPKQMKALNKIFGSLFMLVGALLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 KNVFVQGVIVSVLNPKVALFFLSFLPQFIDTSSGSASMQLLWLGLLFSVLVTMCNILYAS
                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 57; Conserva
ALWIKGPKOMKALNKIFGSLFMLVG-ALLASARHA
                                             RQEFLVAAGNPKAILIFTAFLPQFVDPGQPLGAQFAQLGAAFLLLEWLAIALYSYAGLHL
                                                                                         QRAVEVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRI 171
                                                                                                                                                                                                                                                                                WFAYLLTSIILTLSPGSGAINTMTTSLNHGYP----AGGVYCWASDRTGDSYCAGW----
                                                                                                                                       ASGLALVLHTSAWLFLAIKLLGAAYLLWLAVQLWRT----DAQPLANEASPARPSLWRLG
                                                                                                                                                                                  -RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRR-----HLF 111
                                                                                                                                                                                                                                  WALFVPACFALNLAPGPNNLLSLNNAARHGFATASLAGGGRLLA-----FAGMLALA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGSWVFSRPNSQRYSRGLEGVSGVL--LIG--LAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTLEWWFAYLLTSIILTLSPGSGAI----NTMTTSLNHGYPAG-GVYCWASDRTGDSY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTLAASLGLSAIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWR---GGSTLKVSESVESD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDLNSLLLFIVACLAINMIPGPDVIYIVSNTMKGKLVTGFKAAMGL-----GVGYFV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.5%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                 17.0%;
26.5%;
                                                                                                                                                                                                                                                                                                                            ; Score 180.5; DB 2; Pred. No. 6.9e-10; 34; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID: g9949822; PIDN: AAG07053.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                              97;
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                                                                                                                                                                                                                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic
                                                                                                                                       112
                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hickey,
; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
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C;Species: Pseudomonas aeruginosa (strain PAOL)
C;Species: Pseudomonas aeruginosa (strain PAOL)
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83051
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor A; Reference number: A82950; MUID:20437337
A;Accession: F83051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STOO
A;Cross-references: GB:AE004889; GB:AE004091; NID:g9951014; PIDN:AAG08143.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Gene: PA4757
C;Superfamily: hypothetical protein b1798
A;Cross-references: GB:AE004079; GB:AE003849; NID:g9107960; PIDN:AAF85515.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, Bueno, M.R.P.; Camargo, A.A.; Facincani, A.P.; Ferreira, A.J.S.; as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid transporter XF2730 [imported] - Xylella fastidiosa (strain 9a5c) C:Species: Xylella fastidiosa C:Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-213 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The genome sequence of the plant pathogen A; Reference number: A82515; MUID: 20365717
A; Note: for a complete list of authors see reference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: C82523
R; anonymous, The Xyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
C82523
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                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: C82523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; anonymous, The Xylella fastidiosa Nature 406, 151-157, 2000
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Best Local S
Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \tt ALGVASLLKAEPMLFIGLKYLGAAYLFYLGVGMLRGAWRKLRNPEATAAQAEQVDVHQPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRAVEVNLTNPKSIVELAALFPQFIMP--QQPQLMQYIVLGVTTIVVDIIVMIGYATLAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 180.5; DB 2;
Pred. No. 7.2e-10;
""smatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                          reference number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xylella
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                                                                RESULT
C82139
        conserved hypothetical protein
C; Species: Vibrio cholerae
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                                                                                                   Qγ
                                                                                                                                                                      Qy
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                                                                                                                                         Дδ
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U04992; NID:g451649; PIDN:AAA19047.1; PID:g451652 C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kwon, D. H.; Lu, C.D.; Walthall, D.A.; Brown, J. Bacteriol. 176, 2532-2542, 1994
A;Title: Structure and regulation of the carAB A;Reference number: A55580; MUID:94222830
В
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                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-216 < KWO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pseudomonas aeruginosa
C;Date: 25-Aug-1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein (carA 3' region) -
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ISTVLKEYPSIYTGLQGIGAAYLLYIAYLSWPRQNASNQTPTASRSSYTGTFIQGVLINL 132
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                                                                                                                                                               WRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSR-----RHL 110
                                                                                                                                     ALGVASLLKAEPMLFIGLKYLGAAYLFYLGVGMLRGAWR-KLRNPEATAGQAEQVDVHQR 119
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                                                                  FRQALLLSLSNPKAILFFISFFIQFVDPGYAYPGL-SFLVLAVILELVSALYLSFLIFTG
                                                                                                   FQRAVFVNLTNPKSIVFLAALFPQFIMP--QQPQLMQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                                                           DFW-TYVLGVVFVILLPGPNSLFVLATSAQRGVATGYRAACGVF-----LGDAVLMLLS 60
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27.9%;
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25.0%;
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                                                                                                                                                                                                                                                                                                  Score 178.5;
Pred. No. 1.
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Pred. No. 1.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                              Gaps
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                                                                  178
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VRLAAWFRRRQRLAAGATSGVGALFVGFGVKLATA

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VC1939

[imported] - Vibrio

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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Accession: C82139
C;Accession: C82139
R;Heidelberg, J.F; Eisen, J.A; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: C82139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
Search completed: May Job time: 342 sec
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A; Gene: VC1939
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                                                                                                                                                                                                                                                                                                                                                      109 HLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                  : : : : : ||:| || || || 203
                                                                                                                                                                                                               169 QRIALWIKGPKQMKALNKIFGSLFMLVGALL 199
                                                                                                                                                                                                                                                                                                  113 GLLVQGFVTAIANPKGWAFMVSLLPPFIDQSLSLAPQLTVLVAIILLSEFISMSLYATGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                           69 IA-----FEVLKWAGAAYLIWLGIQQWRAAG--AIDLKSLASTQ-SRR 108
:| | :| ||:||:||:||:| ||:|::::: | |
53 VAVSAVVGIAAVMLRYPDIFTLFKIVGASYLVYLGVQMWRSRGKLAINIEQENTYQGSDW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 FIPTFFFVSITPGMNMTLALTLGMSVGY------RRT----LWMMVGELLGVAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 YLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGTLFSRSV 68
                               6, 2001, 14:40:01
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Result
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Perfect score:
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Maximum Match 100%
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                   "A 460 kb DNA sequence of the Escherichia coli K-12 corresponding to the 40.1-50.0 min region on the lin DNA Res. 3:379-392(1996).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-I- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                          Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                           Duesterhoeft A., Ehrlich S.D.;

"Sequence of the Bacillus subtilis genome region the lev operon reveals two new extracytoplasmic followerse sigma factors SigV and SigZ.";

Microbiology 143:2939-2943(1997).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTE-
-!- SIMILARITY: BELONGS TO THE RHT FAMILY.
This SWISS-PROT entry is copyright. It is produced through a obtween the Swiss Institute of Bioinformatics and the EMBL
                                                                                       Sorokin A., Bolotin A., Purnelle Duesterhoeft A., Ehrlich S.D.;
                                                                                                                                               Kunst F., Ogasawara N.,
Submitted (NOV-1997) to
                                                                                                                                                          Kunst F.,
                                                                                                                                                                    STRAIN-168;
                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK---SLASTQSRRH--L 110
                                                                                                                                                                                                                                                                                                                                                                   RIALWIKGPKQM-KALNKIFGSLFMLVGALLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEWWFAYLLTSIILTLSPGSGAI----NTMTTSLNHGYPAG-GVYCWASDRTGDSYC--A
                                                                                                                                                                                                                                                                                                                                                 FVTQYIRTKKKLAKVGNSLIGLMFVGFAARLAT
                                                                                                                                                                                                                                                                                                                                                                                   FKRALILSLTNPKAILFYVSFFVQFIDVNAPHTGISFFILAATLELVSFCYLSFLIISGA
                                                                                                                                                                                                                                                                                                                                                                                                       FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                          AWAGVATLIKTTPILFNIVRYLGAFYLLYLGSKILYAT----LKGKNSEAKSDEPQYGAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                             FROM
                                                                                                                             OF 1-141 FROM N.A.
                                                                                                                                                                                                                                                (Rel.
(Rel.
(Rel.
(Rel.
L 23.4
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                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                STANDARD;
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36,
37,
KDA
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28.6%;
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
PROTEIN IN AAPA-SIGV INTERGENIC
                                                                                                                                                                                                         Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                the
                                                                                                                                                         Yoshikawa H.,
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EMBL/GenBank/DDBJ
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342E0DF348C9AD9A CRC64;
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                                                                                                Hilbert H.,
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                                       PROTEIN
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databases
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                                      (POTENTIAL)
                                                                           the vicinity
                                                                                                                                                                                                                                               REGION
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 a collaboration -
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European Bioinformatics

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YBF7_PSEAE
P38102; Q9HV45;
01-OCT-1994 (Rel
01-OCT-2000 (Rel
01-OCT-2000 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG12304; yrhP.
           MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J. Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE=94222830; PubMed=8169201;
KWON D.-H., Lu C.-D., Walthall D.A., Brown T.M.,
                                                                                                                                                                                                                                                       Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                       aeruginosa
                                                                                                                                                                               Kwon D.-H.,
Abdelal A.T
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                     STRAIN-PAOL
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                              2
                                                                                                                                                      "Structure and regulation of the carAB operon in aeruginosa and Pseudomonas stutzeri: no untransla
                                                                                                                                                                                                                                                                                              Pseudomonas
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                                                                                                                                          Bacteriol. 176:2532-2542(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIKGPKQMKALNKIFGSLFMLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDL------KSLASTQSR--RHLFQR 113 : ::||| | ::||: | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR-----GVGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                               WMKNSKFQKVFQKITG--IILVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVFVNLTNPKSTVFLAALFPQFIMPQQPQLMQYTVLGVTTTVVDITVMIGYATLAQRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIAKSVILFTTIKYLGAAYLIYLGVKSFFAKSMFSLDDMQSQAKNMASSPKRYYKTSFMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYIPIAAMMVIIPGADIMLVMKNTLRYG-PKAGRYNILGLATGLSF---WTVIAILGLSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSLSNILNPKTVLVYVTIMPQFINLNGNINQQLIILASILTLLAVLWFLFLVYIIDYAKK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z99117; CAB14652.1; U93874; AAB80873.1;
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yro; IPR001123; ..
PF01810; LysE; 1.
POTENT:
POTENT:
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 genome
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                                                                                                                                                                                                                                                                                              aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
 sequence of Pseudomonas
                                                                                                                                                                                                                                                                                                                                  30,
40,
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70
95
175
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27.6%;
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Pred.
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                                                                                                                                                                                                                                                                                 subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195;
No. 2.
                                                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                      untranslated region exists.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                     AA
  aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                    Pseudomonas
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YG27_SYNY3
ID YG27_SYNY3
ID YG27_SYNY3
AC P74343;
DT 01-NOV-1997
DT 01-NOV-1997
DT 15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; TRANSMEM 12 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakai Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura 'Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Yasuda M., Tabata S.;
                                                                                                                          Synechocystis
Bacteria; Cyan
                                                                                                                                                  SLR1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                         MEDLINE=97061201;
                                                                                     SEQUENCE
                                                                                                                                                                HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                             NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                                                                      ALGVASILKAEPMLFIGLKYLGAAYLFYLGVGMLRGAWRKLRNPEATAAQAEQVDVHQPF
                                                                                                                                                                                                                                                                                                                                                                                                    WRGVGTLESRSVIAFEVLKWAGAAYLIWLGIQQ----WRAAGAIDLKSLASTQSRRHL-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                       DFW-TYVLGVVFVILLPGPNSLFVLATSAQRGVATGYRAACGVF-----LGDAVLMLLS
                                                                                                                                                                                                                                                                                                               RIALWIKGPKOMKA-LNKIFGSLFMLVGALLASA
                                                                                                                                                                                                                                                                                                                                        RKALLLSLSNPKAILFFISFFIQFVDPGYAYPGL-SFLVLAVILELVSALYLSFLIFTGV
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                                                                                      FROM
                                                                                                                            Cyanobacteria;
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48
74
134
156
191
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L 22.0
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                                                                                                                                                                                                                            STANDARD;
                                                                          PubMed=8905231;
                                                                                                                                                                35,
36,
36,
KDA
                                                                                                                                       (strain
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68
94
154
176
211
109
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28.0%;
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                                                                                                                                                             Last sequence uplast annotation PROTEIN SLR1627.
                                                                                                                                                                                                   Created)
                                                                                                                             Chroococcales;
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                                                                                                                                       PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
A -> G (IN |
P -> R (IN |
P -> Q (IN |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.5; DB 1;
Pred. No. 5.3e-10;
1; Mismatches 90;
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                                                                                                                                       6803)
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> R (IN REF. 1).
-> Q (IN REF. 1).
A30A08E714591B8D
  the unicellular cyanobacterium
                                                                                                                                                                                                                            206
                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                202
                                                                                                                            Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 216;
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                                                                 Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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RESULT 6
YAHN_ECOLI
ID YAHN_E
AC P75693
DT 01-NOV
DT 115-JUI
DE HYPOTH
GN YAHN.
OS Eschei
OC Eschei
OC Bactei
OX NCBL_1
RN [1]
RP SEQUEI
RA Riley
RA Riley
RA Grego
R
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Best Local :
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
HYPOTHETICAL 24.8 F
      Federspiel N.,
                             Duncan M.,
                                                 SEQUENCE FROM N.A.
                                                                                            Science
                                                                                                                                                  Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch C.A., Per
Riley M., Collado-Vides J., Glasner J.D., Rode
                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               Bacteria; P
Escherichia
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TRANSMEM 47 6:
TRANSMEM 74 9.
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                                                                                                                                B., Shao Y.;
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                                                                                     complete genome sequence nce 277:1453-1474(1997).
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53; Conservative
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    Araujo R.,
R., Kalman
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9 POTENTIAL.
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Pred. No. 6.9e
31; Mismatches
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S., Komp
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C., Kurdi
                                                                                                                                                    Goeden
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ode C.K., Mayhew G.F.,
eden M.A., Rose D.J.,
                                                                                                         coli
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Chung
urdi O.
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[2]
                                                                               The
               SEQUENCE FROM N.A
                                                                                                                       Escherichia coli.
                                                                                                                                                                 Nashimoto H.;
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12;
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                                                                                                                                        Non-ribosomal proteins
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-!- SIMILARITY: BELONGS TO THE RHT FAMILY.
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                                                           York
                                                                             translational apparatus,
                                                                                              erichia coli.";
Nierhaus K.H. (eds.);
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PROTEIN IN SRMB-UNG INTERGENIC
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2 POTENTIAL.

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3 LRLITEGVTOR -> VA (IN REF.)
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                                                                             Plenum
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TRANSMEM 47 67
TRANSMEM 71 91
TRANSMEM 142 162
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Unpublished observations (AUG-1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                 CAGISFSLAVIDPAAVHLLSWAGAAYIVWLA--
                                                                                                                                                                              GVGTLFSRSVI----AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAV
                                                                                                                                                                                                          AFWTYTLITAMTPGPNNILALSSATSHGF------
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D64044; -; NOT_ANNOTATED_CDS.
AE000344; AAC75631.1; -.
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nce 277:1453-1474(1997).
                                                   LAGHLFQRLFRQYGRQLNIVLALL
                                                                           KGPKOMKALNKIFGSLFMLVGALL 199
                                                                                                     ALQFVNVKIILYGVTALSTFVLP-QTQALSWVV-GVSV----LLAMIG--TFGN--VCWA
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ne; EG12445; yfik.
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MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burla
"Analysis of the Escherichia coli ge
from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
[2]
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15-JUL-1998
15-JUL-1999
                                                           EMBL;
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                      EcoGene; EG11468; rhtC InterPro; IPR001123; -
                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        amino acid efflux.";
FEBS Lett. 452:228-232(1999).
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Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RR
Gregor J., Davis N.W., Kirkpatrick H.A., Gov
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              Pfam; PF01810;
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                                                                                                                                                                                                                                                                                                                                  "The novel transmembrane Escherichia coli proteins
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Livshits V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Irino N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS.
                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN SIMILARITY: BELONGS TO THE RHT FAMILY. CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAINTRODUCED IN POSITION 80 TO PRODUCE THIS ORF.
                                                                                                                                                                                                                  CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 47 AND 73.
                                               #87049; AAA67619.1; ALT_FRAME.
#AE000458; AAC76826.1; ALT_FRAME.
##30198; ", NOT_ANNOTATED_CDS.
##30713; S30713.
                                                                                                                                                                                                                                                                                             FUNCTION: CONDUCTS THE EFFLUX OF THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            o N., Nakayama K., Nakayama H.
recQ gene of Escherichia coli
ence for SOS regulation.";
Gen. Genet. 205:298-304(1986)
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                                                                                                                          http://www.isb-sib.ch/announce/
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RESULT 9
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DC CHEMOT
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                                             use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
"Identification, molecular cloning and sequence analysis of a general cluster encoding the class II fructose 1,6-bisphosphate aldolase, phosphoglycerate kinase and a putative second glyceraldehyde 3-phosphate dehydrogenase of Escherichia coli.";
MO1. Microbiol. 3:723-732(1989).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-i- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
         entities requires a or send an email to
                                  modified
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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                             "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                      Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Per
Riley M., Collado-Vides J., Glasner J.D., Rode
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAINE=97426617; PubMed=9278503;
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         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF01810; LysE; 1.
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nitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALWIKGPKQMKALNKIFGSLFMLVGALLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVNLTNP----KSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U28377; AAA69090.1; -. AE000375; AAC75960.1; -. X14436; CAA32607.1; -.
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                                                                                                                                                                                                                                                                                                           salmonicida
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KDA
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24.9%;
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Last annotation update)
PROTEIN IN ASAR-CDPD INTERGENIC REGION
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           Transmembrane
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Pred. No. 0.0011;
6; Mismatches 9
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
SEQUENCE
                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way most field and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                         Roberts D. Allen E., Araujo R., Aparicio A., Chung E., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. FONCTION: PERMEASE THAT IS INVOLVED IN THE TRANSPORT CYTOPLASMIC MEMBRANE OF PROLINE.
                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                        "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
                                  EMBL; AE000146; AAC73505.1; EMBL; U82664; AAB40158.1;
                                                                                                                                                                                                                                                                                    STRAIN-K12;
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                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGAAALSPWLARGRVQQAIDTIVGLIMLGLALQLASGALLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLAMTLGVTLLNPHVYLDTLMLLGSFGSQFAEPLRP----AFAAGAMLASLVWFYSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VF-----VNLTNP-----KSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYA 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                         an email to license@isb-sib.ch).
                                                                                                                                        the Swiss Institute of Bioinformatics
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    35, Created)
    35, Last sequence upon
    35, Last annotation of the properties

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ECOGene; EG13609;

InterPro;

IPR002027;

PF00324;

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P37460;
01-OCT-1994
01-NOV-1997
30-MAY-2000
                                                     This
                                                                 Liao M.K., Gort S., Maloy S.;
"A cryptic proline permease in Salmonella typhimurium.";
"incrobiology 143:2903-2911(1997).
"In Function: permease That IS INVOLVED IN THE TRANSPORT ACCYTOPLASMIC MEMBRANE OF PROLINE.
"I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER-
"I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER-
"I- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
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                                                                                                                                                   MEDLINE=97453475; PubMed=9308174;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=602;
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                               ween the Swiss Institute of Bioinformatics Institute.
                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEFWFSFFKVATIIIMIVAGFGII--IWGIGNGGQPTGIHNLWSN---GGFFSNGW--LG
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50; Conservative
           non-profit institutions as long and this statement is not removed.
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35, Last sequence 39, Last annotations.
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18.1%;
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94;
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            and for
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                                           collaboration
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       Vrljic M., Sahm H., Eggeling L.;
"A new type of transporter with a new type of
lysine export from Corynebacterium glutamicum.
Mol. Microbiol. 22:815-826(1996).
                                                   MEDLINE=97126810; PubMed=8971704;
                                                             STRAIN=R127
                                                                                                       Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                             Bacteria;
                                                                                                                                      Corynebacterium glutamicum (Brevibacterium flavum).
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                                                                                            NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
LYSINE EXPORTER PROTEIN.
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T 01.NOV-1997 (Rel. 35, Created)

T 01.NOV-1997 (Rel. 35, Last sequence update)

J5-JUL-1998 (Rel. 36, Last annotation update)

""DOTHETICAL PROTEIN HI1307.
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STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherry B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fehrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                     Science
                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria;
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                                                                          "Whole-genome random sequencing and
influenzae Rd.";
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TIGR; HI1307;
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                                                                                                                                                                                                                                                                                   Hypothetical
174
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                                                                                                                                                          Local
                      AQRIALWIKGPKQMKALNKIFGSLFMLVGALL
                                             GLLVNLSNAKVVVYFSSVM-SLVLVNITEMWQ-IILAFAVIVVETFCYFYVISLIFSRNI
                                                                                             GLAVLFVTIPALHGVIMLLGGSYLAYLGFLMARSKKYAKFESHSDTEFNQQTTIKKEILK 115
                                                                                                                   GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHL-----FQR 113
AKRLY-----SQYSRYIDNMAGIVFLFFGCVL
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                                                                    AVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVD-----IIVMIGYATL
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                                                                                                                                              l Similarity 21.1
32; Conservative
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66 86
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Search completed: Job time: 191 sec мау 6, 2001, 14:41:20

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2: sp_bacteria:
3: sp_fungi:*
4: sp_human!:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_plage:*
10: sp_plage:*
11: sp_rodent:
12: sp_unclass:
13: sp_vertebr:
14: sp_virus:*
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0916n6 salmonella 09kvk7 vibrio chol 09kvk7 vibrio chol 09rsx2 deinococcus 09r6f8 agrobacteri 09kf9 bacillus ha 09r6j5 agrobacteri 09ks40 vibrio chol 09km3 vibrio chol 09km7 bacillus an 09pp20 xylella fas 09kg9 vibrio chol 05x934 shewanella 09k18 vibrio chol 05x13 shewanella 09k18 streptomyce 0916n7 salmonella me 0916n7 salmonella me 0916n7 salmonella me 0916n7 salmonella
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ALIGNMENTS

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01-0CT-2000 (TrEMBLrel. 1
01-0CT-2000 (TrEMBLrel. 1
01-0CT-2000 (TrEMBLrel. 1
                                                                                                                                                 Waterston R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF233324, AAF33432.1;
SEQUENCE 206 AA; 22322 MW; E089B357D30750F2 CRC64;
                                                                                                                                                                                                                   "The Salmonella typhimurium Submitted (FEB-2000) to the
                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-SGSC1412;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SGSC1412;
                                                                                                                                                                                                                                                                                    Salmonella
                                                                                                                                                                                                                                                                                            Salmonella typhimurium LT2.
Bacteria; Proteobacteria; gamma
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                        MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGYYCWASDRTGDSYCAGWR-- 58
                                                                ### MTFEWWFAYLLTSTLLSLSPGSGAINTWTTSINHGY-RGAVASIAGLQTG----LGIHIV 55
                                                                                                     165;
                                                                                                              Similarity
                                                                                                     Conservative
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                                                                                                    77.2%; Score 819.5; DB 2; 78.2%; Pred. No. 5.3e-65; tive 15; Mismatches 20;
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15,
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01-0CT-2000 (TYEMBLZel. 15, La
01-0CT-2000 (TYEMBLZel. 15, La
нуротнетісац ряотеім VC0136.
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OSRSX2:
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O1-MAY-2000 (TIEMBLITE1. 1
O1-MAY-2000 (TIEMBLITE1. 1
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O1-JUN-2000 (TIEMBLITE1. 1
CONSERVED HYPOTHETICAL PF
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TIGR; VCC
SEQUENCE
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                     Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
EMBL; AE004104; AAF93313.1; -.
TIGR; VC0136; -.
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STRAIN-EL TOR N16961
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                    NIMTRMNKLFGSMFMGCGMLLATAK 204
                                                                                                                                                                                                                                                                                                                                                                          KOMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                   LTNPKSIVELVALFPQFIDPTRDHWPQFLVLGITTVTIDAIVMFGYTALAAQLGRYIRSP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                          LTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWIKGP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIGALVAQSALAFTLIKWIGAAYLVWLGIQKWRDRAPLTATTTSHELSQAALLRKAVLIN 119
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89; Conser
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13, Last sequence update)
14, Last annotation update)
PROTEIN.
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Last sequence update)
Last annotation update)
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Pred. No. 3.3e
14; Mismatches
                                                           group;
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                                                             Deinococcales;
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Best Local
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                          STRAIN-MAFF301001;
SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
"Novel structural difference between nopaline- and octopine- type
gene:construction of genetic and physical map and sequencing of
trb/traI and rep gene clusters of a new Ti plasmid pTi-SAKURA.";
Biochim. Biophys. Acta 1396:1-7(1998).
                                                                                                                                                                                    Gene
[2]
                                                                                                                                                                                                                                                                                                                                                                   Plasmid pri-SAKURA.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Agrobacterium,
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INTERPRO; IPRO01133; -.
PFAM; PFO1810; LYSE; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATD; UNKNOWN_1.
SEQUENCE 241 AA; 25161 MW; A4017ABFEDB60374 CRC64;
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Science 286:1571-1577(1999).
EMBL; AE002037; AAF11548.1;
                                                                                                                                                                                                       Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K., Katoh A., Yoshida K.; Katoh A., Toshida K.; "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid."; Gene 242:331-336(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9R6F8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20036896; PubMed-10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Elsen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Felschmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-MAFF301001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens
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                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=362;
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radiodurans R1.";
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54; Conservative
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; Pred. No. 1.1e-12,
41; Mismatches 8
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Last sequence update)
Last annotation update)
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Q9KFP9;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                    SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Taka
Submitted (MAR-2000) to the
EMBL; AP001508; BAB04148.1;
                                                                                                                                                           Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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    SEQUENCE
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EMBL; AB016260; BAA87726.1; -.
INTERPRO; IPR001123; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., "Genome structure of pri-SAKURA(I): Strategy for DN Japanese cherry-Ti plasmid."; Nucleic Acids Symp. Ser. 37:159-160(1998).
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                                                                     Takaki Y.
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Pred. No. 6.7e-10;
4; Mismatches 83;
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Best Local S
Matches 57
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SEQUENCE FROM N.A.
STRAIN-MAFF301001;
Uraji M., Suzuki K., O
Uraji M., Suzuki K., O
STRAIN-MAFF301001;
                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                        Ohta
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Katoh A., Yoshida K
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                 Nucleic Acids
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Rhizobiaceae; Agrobacteri
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"Complete nucleotide se
Gene 242:331-336(2000).
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                                                                                                                                                                                                                                                                                                                             "Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh i "Genome structure of pri-SAKURA(I): Strategy for Japanese cherry-Ti plasmid.";
Nucleic Acids Symp. Ser. 37:159-160(1998).
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57; Conserv
                                                                                                                                                                                               Acids
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                                                                                                                                                                                                                                        Suzuki K.,
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Agrobacterium.
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                                                             Ohta N., Hattori Y., Katoh A., YopTi-SAKURA (IV): Characteristics Ser. 39:187-188(1998).
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Last annotation updat
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Pred. No. 1.2e-09;
0; Mismatches 87;
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of
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Nucleic
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB016260; BAA8768: INTERPRO; IPR001123; -. PFAM; PF01810; LySE; 1.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of both cholerae.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=666;
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                                                                         MVIQNFEAFFIAITILTLTPGLDTALVIRNTSRAGFADG---C---TTSLGICFGLFVH
                                                                                                                       MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW---
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B016260; BAA87689.1; -.
                                                                                                                                                                                                 Similarity
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RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRA----AGAIDLKSLASTQSRR 108
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0 (TrEMBLrel. 15,
aL PROTEIN VC1421.
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27.4%;
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23.6%;
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Last annotation update)
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Pred. No. 1.4e-09;
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No. 2
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Q9XBR8
ID Q9
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DT 01
DT 01
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I.
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Selle
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White
McDonald C., Smith H.O., Colwell R.R., Mekalanos J.J., Venter
                                      Q9XBR8;
Q9XBR8;
Q1-NOV-1999
Q1-NOV-1999
Q1-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KMJ3;
01-OCT-2000
01-OCT-2000
01-OCT-2000
              HYPOTHETICAL ZM10ORF7.
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 Zymomonas mobilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of both chromosomes
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                                                                                                                                                                VGSWVFSRPNSQRYSRGLEGVSGVL-
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                                                                                                                                                                                                                                                                         HTLAASLGLSAIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWR---GGSTLKVSESVESD
                                                                                                                                                                                                                                                                                                 -- CAGWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQ----QWRAAGAIDLKSLASTQSR 107
                                                                                                                                                                                                                                                                                                                             MDLNSLLLFIVACLAINMIPGPDVIYIVSNTMKGKLVTGFKAAMGL-----GVGYFV
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                                                    sequence
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No. 4.7e-09
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01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                Okinaka R.T., Cloud K., Hampton O., Kumano S., Manter D., Martinez Y., Brown A.E., Jackson P.J.;
                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1392;
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Okinaka R.T., Cloud
                                                                                                                                                                                                                                                                                                                                                                                                   Q9RMX0
                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                    INTERPRO
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                         Plasmid
                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                               PX02-63
                                                                                                                                                                                                                                                                                                                                                                                        Q9RMX0;
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    113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 LLRFLKRPRFLSVIDRLTGCVFIAFGLKIALSK 156
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                                                                                     1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAG-GYYCWASDRTGD----SYCA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.W., Kang
he sequence
                                                               MDLNIWITVLLVGTIGVISPGPNWAVIIKNSL---YSRSLGVSTVAGIATGSLIHIVYCL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQ-----QWRAAGAIDLKSLASTQSRRHLFQR 113
RAVEVNLTNPKSTVFLAALEPQFIMPQQPQLMQYIVLGVTTIVVDII----VMIGYATLAQ 169
                     --IGIGVIISKSILLFNTLKWIGVAYLLYIGIKLLRSKKQSPAAIIKNNESTTWK--AFR 113
                                   --LWIKGPKOMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt GLGAVLRASELAYNLIKWSGAAYLCWLGINLLIHPRKNLVDNLDPSMPSATKALRQGF---}
                                                                                                                                                                                     νκυ; ινRUU1123; -.
PF01810; LysE; 1.
                                                                                                                                                                                                 tted (NOV-1999) to the AF188935; AAF13668.1; PRO; IPR001123; -.
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AF157493; AAD4:
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analysis
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                                                                                                                      Score 184; DB 2
Pred. No. 7e-09;
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Pred. No. 4.
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Coulombo C., Costa F.F., Carraro D.M., Carrer H.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Coutinho L.D., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.Y.F., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Machado M.A., Mattins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Machado M.A., Mattins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Monn J.H., Nagai M.A., Nascimento S.L.T.O., Netto L.E.S.,
RA Moin A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Deixolo R.B., Dereira G.A.G. Dareniera J.A., Paris A.,
RA Deixolo R.B., Dereira G.A.G. Dareniera J.A.,
RA Deixolo R.B., Dereira M.D., Dareniera J.A.,
RA Deixolo R.B., Dereira M.D., Dareniera J.A.,
RA Deixolo R.B., Dereira M.D., Dareniera J.A.,
RA Deixolo R.B., Dereira M.D., Dareniera J.A.,
RA Deixolo R.B., Dereira M.D., Dareniera J.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE004079; AAF85515.1; INTERPRO; IPR001123; -.
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213 AA; ;
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TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-EL TOR N16961 / SEROTYPE 01; MEDLINE=20406833; PubMed=10952301;
                                                             Shewanella colwelliana (Alteromonas Bacteria; Proteobacteria; gamma subc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salzberg S.L., Smith H.O., Fraser C.M.;
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                   NCBI_TaxID=23;
                                             Shewanella.
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(TrEMBLrel. 15,
L PROTEIN VC1939.
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26.1%;
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14,
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Last annotation
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Pred. No. 2.7e
35; Mismatches
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                                                                  subdivision;
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.7e-07;
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                                                                  Alteromonadaceae;
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RESULT
Q9KLA0
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Q9K775;
Q9K775;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DIHYDRODIFICOLINATE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuqua W.C., Weiner R.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X67020; CAA47413.1;
INTERPRO; IPRO01123;
PFAM; PF01810; LysE; 1.
SEQUENCE 153 AA; 16579 MW; A9F3167C965BB34F CRC64;
                                                                                                                                                                                                                                                                                                                               STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Tubmitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AP001519; BAB07214.1; -
SEQUENCE 208 AA; 23158 MW; CAD7A46D63B8E4
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=D;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL
                                                                                                                                                                                       VIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTNPKSIVF
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                                                                                                                                LAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIV--MIGY--ATLAQRIALWIKGPKQMK 182
                                                               YMNIAATIIFIGLGLKLMTTQ
                                                                                    ALNKIFGSLFMLVGALLASAR
                                                                                                             YLTFLPQFVNYQSANISLQLCILGLIFIIMTAIIFSIFGYFSGTFRDRL----LKNSRFNE
                                                                                                                                                                 VVVFTIFKLAGAMYLFYLAYKALKHRKEEIRVNSEKTNDLKGLFLRGLIMNVLNPKVAIF 129
                                                                                                                                                                                                                  FMGSAIMLIIIPGPDLVFTITQGMTNGRKAGVITAMGLSLGNIVHTLAAVLGLSLIIQTS
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Pred.
                                                                                                                                                                                                                                                                   Score 154.5; DB 2;
Pred. No. 2.8e-06;
4; Mismatches 100;
   PRT;
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ພາດ. 1.8e-06;
51
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Search completed: May
Job time: 246 sec
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Best Local Similarity 2/...
Matches 46; Conservative
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDILINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000).
EMBL; AE004412; AAF96744.1; -.
TIGR; VCA0846; -.
SEQUENCE 204 AA; 21719 MW; D09887299659FBBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCA0846.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                            \ensuremath{^{\text{TDNA}}} sequence of both chromosomes of the cholera pathogen Vibrio cholerae. \ensuremath{^{\circ}}\xspace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                 115 ---EGLLISLLSPKIALFFIALFSQYVAVGS-DLTSKAAIVITPLVVD 158
                                                                                                     57
                                                                                                                                                      56 ITLIGLAVVLHQSPVLFKTISYAGAAYLAYLGWNALRSKGGVAAKLESGESVSVWQSAR- 114
                                                                                                                                                                                                                        —
                                                                                                                                                                                                                                                     1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAG---- 56
                                                                                                                                                                        --WRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK-----SLASTQSRRH 109
                                                                                                                                                                                                                      MTLTVWLSLFTICILGAMSPGPSLAMVAKHSLAGGRKNGFAAAWA-----HAFGIGVYAF 55
                                                                                                                                                                                                                                                                                                        13.5%;
                  2001, 14:40:50
                                                                                                                                                                                                                                                                                    5%; Score 143.5; DB 2;
4%; Pred. No. 2.6e-05;
27; Mismatches 74;
                                                                                                                                                                                                                                                                                                                        Length 204;
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9b_9ss1:AF095402

9b_est44:AW290151

9b_est96:BG12821616

9b_est96:BG12816

9b_est72:BE334024

9b_est72:AE334024

9b_est73:AW701441

9b_est50:AW701441

9b_est18:A1256819

9b_est14:AA941801

9b_est18:BF493242
                                                                                                                                                                               gb_est83:BF128485
gb_est39:AV651857
gb_est39:AV651904
gb_est3:AA156246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est82:BF043998
gb_est28:AL509238
gb_est90:BF679835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database: EST:*
Database sequences: 9623517
Database length: 73081774
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Query: US-09-466-935-2
Query length: 205
                                                                                                    gb_est69:BE049512
gb_est11:AA735580
gb_est86:BF345786
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gb_est78:BE784988
gb_est88:BF526220
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gb_est95:BG038404
gb_est89:BF614897
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gb_gss24:AZ601442
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-Q-/cgn2_1/USPTO_spool/US09466935/runat_03052001_075709_14787/app_query.fasta_1.529
-Q-/cgn2_1/USPTO_spool/US09466935_runat_03052001_075709_14787/app_query.fasta_1.529
-DB=EST -QFMY=fastab_ -SUFETX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALICK=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTPENT=pfs -NORM=ext -MINLEN-0
-MAXLEN-200000000 -USER-US09466935_@CGN1_1_3199 -NCPU=6
-CCPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
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                                                                                                                                                                                                                                                                                                                 gb_gss7:AQ525982
                                                                                                                                                                                                                                                                                                                                          gb_est88:BF489020
gb_est97:BG172141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss3:AQ240216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_gss5:AQ365906
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227.
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126
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AQ858095 nbeb0011L14f CUGI Rice
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I AC601442 IM0419P08R MOUSE 10Kb
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BF643998 BP250014A20H3 SOATES
I AL509238 AL509238 HOTGeum Vulga
BF69835 602154419F1 NIH_MGC_83
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gb_est28:AL503330
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BASE COUNT
ORIGIN
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ859250 473 bp DNA GSS 03-NOV-1999 nbeb0011L14r CUGI Rice BAC Library (ECORI) Oryza sativa genomic
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A BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 41 High quality sequence stop: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
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Quality:

Ratio:

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Percent Identity:

86.792

Length:

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US-09-466-935-2 x AQ859250/rev
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KEYWORDS
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AUTHORS
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LOCUS BG038404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Pers, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. Washu Xenopus EST project, 1999 Unpublished (1999)
Other_ESTs: d934h08 x1
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2001 (3934h)8.yl Xenopus laevis gastrula non normalized Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:Xlnnga009pl6 5' similar to TR:Q9RSX2 CONSERVED HYPOTHETTORI DECERTED:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPRSX2 CONSERVED HYPOTHETICAL PROTEIN. ;, mRNA sequence. BG038404
BG038404.1 GI:12480989
EST:
                                                                                                                                                                                                                                                                                                                                               Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                  primer: -40RP from Gibco
h quality sequence stop: 430.
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314 286 1810
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/note-"Vector: pBluescript SK-; Site_1: ECORT; Site_2: XhOI; cDNA was prepared from 2ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae). ECORI-XhOI cut cDNA was then ligated into UniZap-XR
                                                                                         /clone="XENOPUS_SOURCE_ID:xlnnga009p16"
/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F'"
                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                          Location/Qualifiers
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SOURCE

ORGANISM

Xenopus

laevis

African clawed

frog

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alignment_block:
US-09-466-935-2 x BG038404
VERSION
KEYWORDS
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                                                                                                                     seq_documentation_block:
LOCUS BF614897
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Percent Similarity:
                                                                                                  DEFINITION
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                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACACGCTGGCTGCCGGCCTTTCGCAGGGGGCGCGGGCGAGCGTCATTG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTACATGGCGTGGAACACGCTGCAGGAGAATGGCGCGCTGAAGATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCCGCATCTGCTCGCCGCCATCACCGGTCTTGCCGCCATCCTGCACAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValT 42
                                                                                                                                                                                                                                                                                                                                                                                                                           SerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPh 116
                                                                                                                                                                                                                                                                                                                                              eValAsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPheP 133
                                                                                                                                                                                                                          CGCAGTTCATCGCGCCGGATGAG
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                                      dg18a02.yl Xenopus laevis gastrula non normalized Xenopus laevis cona clone XENOPUS_SOURCE_ID:Xlnnga005b04 5' similar to TR:Q9RSX2 CONSERVED HYPOTHETICAL PROTEIN. ;, mRNA sequence.
  BF614897.1 GI:11787968 EST.
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a 142 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Stratagene) with EcoRI at the 5' end and XhoI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to COt-omega of 11. After removal of hybrids and
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Percent Identity: 28.369
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alignment_block:
US-09-466-935-2 x BF614897
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                                                                                                                     31 rLeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspA 48
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48 rgThrGlyAspSerTyrCys.......
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Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnnga005b04
Seq primer: -40RP from Gibco
High quality sequence stop: 401.
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Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, M., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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1 (bases 1 to 428)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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314 286 1810
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ECORI-XhoI cut cDNA was then ligated into UniZap-XR (Stratagene) with ECORI at the 5' end and XhoI at the 3' end. SS-library phagenids were prepared by mass excision from the original library and normalized by hybridization to biothnylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagenids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1911 1100). Note that the simple strended control of the strended strended and clectroporated into Top-10 F'.
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/clone_lib="xenopus laevis gastrula non normalized"
/tissue_type="qastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10_F/"
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/db_xref="taxon:8355"
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Percent Identity: 27.407
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 uValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnG :|||:::|||::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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nbxb0064N05f CUGI Rice BAC
nbxb0064N05f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (199 On Dec 15, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wing, R.A. and Dean, R.A.

BAC End Sequencing Framework to Sequence the Rice Genome
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Location/Qualifiers
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small
                                                                                                                                                                              /cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1998)
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ACCESSION
VERSION
KEYWORDS
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US-09-466-935-2 x AQ365906
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                               COMMENT
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                                                                                                                          REFERENCE
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Percent Similarity:
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                                                                           AUTHORS
TITLE
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                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaTyrLeuIleTrpLeuGlyIle 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyAla 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTTCTCCGGGGGGGGGGCGCCATTGCGTCGATGTCCAGTGGTCTGCAGT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGGCGCTGATCGTTCAGATCGCGGATCATCGCCGCAGGCCTGGGTGCCG 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GlyValGlyThrL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .........TGGCGCGGTTACTGGAACGCCCTCGGTCTGCA 438
Contact: Wing RA Clemson University Genomics Institute
                                            Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                AQ858095 769 bp DNA GSS 03-NOV-1999 nbeb0011L14f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0011L14f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                     Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                      GSS.
                                                                                                                                                                   Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                              AQ858095.1 GI:6208552
                                                                                                                          (bases 1 to 769)
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2.534
54.630
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Percent Identity: 27.778
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ACCESSION

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alignment_block:
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                                                                                   seq_documentation_block:
LOCUS AZ576789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 3.500 Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                            34 isGlyTyr 36
                                                                                                                                                                                                                                                                                                                                                       ACGGGTAT
Olal2 Shot-gun genomic library of Rhizobium strain sp. NGR234 genomic clone Olal2, DNA sequence. AZ576789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start:
High quality sequence stop: '
Location/Qualifiers
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100 Jordan Hall, C
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Fax: 864 656 4293
Email: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_nost="E. Coll Drive"
//note="Wector: pBACIndigo; Site_1: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa.

Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
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/clone="nbeb00111.14f"
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3.500
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Gaps: 0
Percent Identity: 91.667
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                                                               ANU265 Rhizobium
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us-09-466-935-2.rst

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/clone="01a12"
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ANU265"
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                                            Rhizobium sp. NGR234.
Rhizobium sp. NGR234
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
1 (bases 1 to 407)
                                                                                                                                                    Viprey V., Resential, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome GenomeBiology.com 1 (6), 0014.1-0014.7 (2000)
Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
Fax: +44(0)1603450045
Fax: +44(0)1603450045
Fax: 1 virginie.viprey@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 CCGCCCTCGCCGCGACGCGGCGATCATGCCAGGCGGCGTGCTGCACACG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 .....CTCTATGCCGCG.....CTCGGCGTCACGTCGTCTTGCATCT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 SerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPh 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 eValAsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPheP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 laGly......GlyValTyrCysTrpAlaSerAspArgThr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 gSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHisGlyTyrProA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GAGGCGGGGGCGAGCTCTCGCGCTGGGCGAGCTTTCGACAGGGGGCGCT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GACGAGCCTGATGAANCCGAAGGCCTATCNCTTCATGTTCGCCGNCTACC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 leTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 4
Percent Identity: 28.148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
    GI:11603030
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1.394
59.259
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                                                                                                                                                                                                                                                                                                                                                                                Class: shotgun.
    AZ576789.1
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AUTHORS
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                                                                                                                                                                                                                          COMMENT
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih, gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.library

Plate: LLAM9649 row: j column: 08

High quality sequence stop: 602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 932)
                                                                                                                                                                                                                                                                                                      BE784988 932 bp mRNA EST 20-OCT-2000 601478429F1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3881191 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 CCTTCTACTTGTGGCTTTAAGAATG......267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 uLeuThrSerIlelleLeuThrLeuSerProGlySerGlyAlaIleAsnT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27, hrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValTyrCys 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 TrpAlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrpArgGlyVa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetThrLeuGlufrpTrp......PheAlaTyrLe 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 233
Gaps: 14
Percent Identity: 24.034
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192 c 259
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US-09-466-935-2 x BE784988
                                                                                                                                                                   seq_name: gb_est78:BE784988
                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                seq_documentation_block:
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Ratio:
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133 roGln 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
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                                                                                    13 CGCAG
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                                                                                                                                                                                                                                                                                                                                           DEFINITION
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101	Source 1	10 BASE COUNT 148 a 198 c ORIGIN	alignment_scores: Quality: 90.50 Ratio: 1.065 Percent Similarity: 43.590	40 alignment_block: US-09-466-935-2 x BF526220	Alig	287	337 GGTGAGGCCTGTAGGCCAAC 39 47 spArgThrGlyAspSerTyr	387	428 GCAGATCTGTCCCTTTGGC 76 palaGlyalaAlaTyrLeuI	477	92	109 HisLeuPheGlnArgAlaVa ::::::	121 nProLysSerIleValPheL a, Euteleostomi; 11	131LeuPhePrc 	144 MetGlnTyrlleValLeuGli::			160 be 715
		laileAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisL 110		.eualaalaLeuPheProGlnPheIleMetProGlnGln 140 ::: .t.GGAGACACACAAAACTGTTGGGGCAACAGATGCTGA 492	ProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleVal 155 :::::: CTCAGCTCCTGAAAACAGTGCTGCACATCATCCAGGTGGTC 539	spilelleValMetile	GlytyralathrLeu167 		roLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191 	3St88:BF526220	tion_block: 774 bp mRNA EST 11 02071233F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone I	. mkna sequence. F526220. F526220.1 GI:11613570	uman. omo sapiens Matryota; Metazoa; Chordata; Craniata; Vertebrata; ammalia: Eutheria: Primates; Catarrhinl; Hominidae;	(bases 1 to 774) IH-MGC http://mgc.nci.nih.gov/. IH-MGC http://mgc.nci.nih.gov/. Altonal Institutes of Health, Mammalian Gene Collected the Co	ontact: Robert Strausberg, Ph.D. el: (301) 496-1550 mail: Robert Strausbergenih.gov	Issue from the manner of the control	DNA Sequencing by: Incyte Genomics, Inc.	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informat found through the I.M.A.G.E. Consortium/LLNL at:

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ref="taxon:9606"

ref="taxon:9606"

ne_"IMAGE:4214263"

ne_"IMAGE:4214263"

nuc__type="glioblastoma with EGFR amplification"

lost="bH10B (T1 phage-resistant)"

Lost="bH10B (T1 phage-resistant)"

2: Sal1; Cloned unidirectionally. Primer: Oligo dT.

age insert size 1.57 kb. Constructed by Life

nologies. Note: this is a NCI_GGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EleuAlaAla.....130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTTCTCTCCTCCCTTCAGACCCATCATTG 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         buLysSerLeuAlaSerThrGlnSerArgArg 108
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FTGTTGTGCGTGTGTGTGAGAGCACATCAGTG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....rccrggcrcccag 727
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|CCAATTGGTGGAGTCTCAGGGTAGCCCAGG 386
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CAATGTCGCCCAGCAGTGAGGGAGTCGGGA 336
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                                                                                                                                                                                                                                                                                                                                                                                                   hrMetThrThrSerLeuAsnHis..... 34
                                                                                                                                                                                                                                                  Length: 195
Gaps: 8
Percent Identity: 25.128
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7 11:08:09 2001

Mon May

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Contact: Olin Anderson
Contact: Olin Anderson
West Area, Western Regional Research Center
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Fax: 510559573
Fax: 5105595818
Email: condersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF202399 438 bp mRNA EST 06-NOV-2000 WHE1768_B10_C202S Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE1768_B10_C20, mRNA sequence.
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Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 leMetProGlnGlnProGlnLeuMetGlnTyrIleValLeuGlyValThr 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33
                                                     ...TrpArgAlaAlaGlyAlaIleAspLeuLys.....SerLe
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328 TTGGGAGGTGGACCAGAATTCTGCACTGGAGGCCTACTCTGCATGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                              146 TGGAACTGCTTGCCCATTAATGAAGGGCTCACCTCCATAATCTTTCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                  112 GlnArgAlaValPhe.....ValAsnLe
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                                                                                                                                                                                                                       uAlaSerThrGlnSerArgArg....
                                                                                                                                                                                                                                                                                                                           BF202999.1 GI:11117741
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/clone_lbs_gvw_vol23
/clone_lbs_gvw_vol24
/clone_lbs_gvw_vol25
/clone_lbs_gvw_vol25
/ds_lbs_gvw_vol26
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/lab_host="E. coli strain XLOLR" it=1: EcoRI; Site_2: /note="vector: pBluescript SR*; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post incculation with Sinorhizoblum meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Glapack III Gold packaging extracts. Plasmids containing cDNA inserts were exclsed from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR sequence name:WTCBW60TK
More information is available at. . http://chrysie.tamu.edu/medicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                             barrel medic.
Medicago truncatula
Bukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta: eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoldeae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
                                                                                                                                                                                                                                                                                                                                  [ (bases 1 to 607) Fredorova, W. Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Pe, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
                                                                     AW980930 607 bp mRNA EST 07-SEP-2000 EST392083 GVN Medicago truncatula cDNA clone pGVN-60123, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ArgThrGlyAspSerTyrCysAlaGly.....Tr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 607
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Gaps: 12
Percent Identity: 22.772
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/cultivar="genotype A17"
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/clone="pGVN-60123"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Carroll P. Vance
                                                                                                                                                                    AW980930.1 GI:8172475
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seq_name: gb_est53:AW980930
                                                seq_documentation_block:
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/crganism="Triticum aestivum"
/cultivar="Chinese Spring"
/dultivar="Chinese Spring"
/dultivar="Chinese Spring"
/dultivar="Chinese Spring"
/clone=lib="Wheat pre-anthesis spike cDNA library"
/clone=lib="Wheat pre-anthesis spike cDNA library"
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/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcorR; Site_2: Xhoi; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, and yellow anther were collected and total RNA, and polly(A) RNA were prepared, a CDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratgene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 hrGlnSerArgArgHisLeuPheGlnArgAlaValPheValAsnLeuThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 eGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerT 104
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225 ACCTACCGGTGACGCCATCTTCTACACCACCGTGCCGGC 274
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6 GACCGGGTACCGGATGCATAT...CAAGGGTGGCGGTCACGCTACTGCTC 52
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Percent Identity: 22.293
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44.586
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                                                                               FEATURES
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (qii4732114) ppl.ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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Dunn,D., Adyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., M., Rose,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                     plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGC1M0419P08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0419 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
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Gaps:
                                                                                                                                                                                     AZ601442 489 bp DNA
1M0419P08R Mouse 10kb plasmid UUGC1M
clone UUGC1M0419P08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
1. .489
                                                                                                                                                                                                                                                                                                  AZ601442.1 GI:11723632
159 IleValMetIleGlyTyrAla 165
                                      372 GIGCIGGAGGICAAGIGGGCC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
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HindIII"
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                   165 a
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Quality:
                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                            alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Was Building
Unpublished (1998)
Other GSSs: CIT-HSP-2385F1.TR.1
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ240216 511 bp DNA GSS 30-SEP-1998
CIT-HSP-2385F1.TF,1 CIT-HSP Homo sapiens genomic clone 2385F1, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Sperm"
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                                                                                                                                                                                                                                                                 245 AGCA......GCAGAGGAAGCGCCCAGGGCGGCGGCTGCAT 208
                                                                                                                                                                                                                                                                                                                                                  207 ACTGGCCGGGGGGGCTCCTTTCTTGTCCTGAGCCCCTCAGGACCTACG 158
                                                                                                                                                                                                                         39 yGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaG 56
                                                                                                                                                                                                                                                                                                                                                                                          ......LeuPheSerArgSerValIleAlaPheGluVa 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 lLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 TTTGCGCGCAGCTGGCAG.....GCTCTGTGGCAGCCCGCGCAGAGGT 65
                                                                                                                                            23 GlyalaIleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                      to: 489
  Percent Identity: 31.522
                                                                                                     Align seg 1/1 to reverse of: AZ601442 from: 1
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                                                                                                                                                                                                                                                                                                          56 lyTrpArgGlyValGlyThr.......
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AQ240216
AQ240216.1 GI:3672414
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US-09-466-935-2 x AZ601442/rev
  50.000
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LOCUS AQ240216
Percent Similarity:
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Funding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing denome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Wonnack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 514)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA EST 10-OCT-2000 normalized bovine placenta Bos taurus cDNA
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346 AGGGATGAAGGAGATCCTTTGCGAGAGGCATGTTCTTGTGTGGGGTAGGTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 GCTCTGCACCAGGCATTTCTTCTTGTTTTCCTCTTCTCCTCTTCTGGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ThrLeuPheSerArgSerVallleAlaPheGluValLeuLys...TrpAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 aGlyAlaAla......TyrLeuIleTrpLeuGlyI 87
                                                                                                                                                                                                                                                                                                                                                                                              18 LeuSerProGlySerGlyAlalleAsnThrMetThrThrSerLeuAsnHi 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 spSerTyrCysAlaGlyTrpArg.....GlyValGly 61
                                                                                                                                                                                                                                                                                                                                           to: 511
                                                                                                                                  Length: 88
Gaps: 6
Percent Identity: 30.682
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114
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121 c
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Unpublished (2000)
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Tel: 217 333 5998
Fax: 217 244 5617
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51.136
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LOCUS BF043998
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source
                                                 AUTHORS
TITLE
JOURNAL
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                                   REFERENCE
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                                                                                                 COMMENT
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Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                seq_documentation_block:

LOCUS AL509238 623 bp mRNA EST 04-JAN-2001

DEFINITION AL509238 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)

ACCESSION AL509238

VERSION AL509238.1 GI:12035741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 resescerrecerracresascresessecrererecererererer 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 TyrCysAlaGlyTrp...ArgGlyValGlyThrLeuPheSerArgSerVa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 LeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHi 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 sGlyTyrProAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 lileAlaPheGluValLeuLySTrpAlaGlyAlaAlaTyrLeuIleTrp.
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 5
Percent Identity: 27.523
FORWARD: TAATACCTCATCATAGGG
BACKWARD: ATTAACCTCATCAAAA
Insert Length: 514 Error: 0.00
Plate: BP250014A20 row: H column: 3
Seq primer: AGGGGGATAACAATTTCACACAGGA
High quality sequence stop: 514.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                             /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                       1.755
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                                                                                                                                                                                                                                                                                                                                                                                        86.00
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US-09-466-935-2 x BF043998
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                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                          83
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KEYWORDS
SOURCE
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/lab_host="XLOLR"
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/lab_host="NLOLR"
/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
Xho1; mRNA was made from developing caryopsis (3.-15.DAP)
of spring barley variety 'Barke', a high quality malting
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(3'-end of CDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the EcoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is I kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp"
26 a 150 c 166 g 179 t 2 others
                                                                                                                                                                                     Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekeipk gatersleben.de, http://pgrc.ipk-gatersleben.de Seq primer: Mi3uni primer for 3'end.
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"
                                              Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A. EST sequencing and analysis in barley
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||:::::: ||| ||| ||||||::||||
110 CCTGGCGCCAGCTACATCATCACTACAACCCTTCCTGCGTTTGC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....TACTGCTCG 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
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Gaps: 6
Percent Identity: 27.523
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                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Barke"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="HY01C09u"
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44.037
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US-09-466-935-2 x AL509238
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seq_name: gb_est90:BF679835	45 aSer
seg_documentation_block: LOCHS RE679835 977 bp mPNA RST 21-DEC-2000	424 CTCGGCCTTGTCAT
602154419F1 NIH-MCC_83 Homo sapiens CDNA	TACGCGGCA
N N SS	60 ValGlyThrLeuPh
SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	524
	:::
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D.	92 aAla 579 GGCGAAGCTCAAGC
Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: CLONETECH Laboratories, Inc.	98 euLysSerLeuAla
CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.	629 TGGGTAGTGCAGCC
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	664
Plate: LLCM1146 row: e column: 06 High quality sequence stop: 674.	131 uPheProGlnPheI
FEATURES Location/Qualifiers source 1, 977	699 grrccraggraga
Site_1: Sfil (grocectogoc); Site_2: Sfil (grocattatggc); 5; and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC'3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGGCGGCGCCGCAGTGATGODSN-3' (where B = A, C, or G and N = A, C, G, or T). Average	
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech	
BASE COUNT 159 a 289 c 311 g 218 t .	
alignment_scores: Quality: 86.00 Length: 184 Ratio: 1.049 Gaps: 11 Percent Similarity: 44.565 Percent Identity: 25.543	
alignment_block: US-09-466-935-2 x BF679835	
Align seg 1/1 to: BF679835 from: 1 to: 977	
3 LeuGlurrpTrpPheAlaTyrLeuLeuThrSerllelleLeuThrLeuSe 19	
19 rProGlySerGlyalalleAsnThrMetThrThrSerL 32	
32 euAsnHisGlyTyrProAlaGlyGlyValTyr.CysTrpAl 45	

45	aser	46
424	CTCGGCCTTGTCATCCTCCACAAAGAGCAGCTTGGCAAAGCCCACCTGGT	473
47		59
474	474 TACGCGGCATGGGCAGGCTGCTGCTGTGCTGTGTGGGCAGGCTGTGCA	523
09	60 ValGlyThrLeuPheSerArgSerValIleAlaPheGluValLeuLySTr	92
524	TITITITITITITITITITITITITITITITITITITI	534
16	palaGlyalaala.Tyr.LeuIleTrpLeuGlyIleGlnGlnTrpArgAl	92
535	GGGTGGGGCTGCTCCCCAAGCTGGTTGCCCCGATGGCCCCT	578
92	aAlaGlyAlaIleAsp	86
579	GGCGAAGCTCAAGCTATACCATGCTACTTCTGGGCTGGTGGGCTACCTGC	628
86	euLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAla	114
629		663
115	ValPheValAsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLe	131
664	TCTGGTTCACTGTCTCTGTCACTGGGTGCAGCCTG	698
131		
669	GITCCCTGGGTGGTTTATGCCCTGGTCTCACCTGGTTGGTCATAT 744	

Run on:

Title:

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AX030177 Sequence
AE000458 Escherich
AE005613 Escherich
AC073768 Mus muscu
AC020970 Mus muscu
AC020916 Mus muscu
AC079167 Mus muscu
AC079167 Mus muscu
AC079167 Mus muscu
AC079167 Mus muscu
AC079167 Mus muscu
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1 atgttgatgttatttctcac......ttcatttgattatttcgcgg 618
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Blattner, F.R.
             Query Match 100.
Best Local Similarity 100.
Matches 618; Conservative
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REFERENCE
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AC020874 Mus muscu
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AE004719 Pseudomon
AE004109 Vibrio ch
AF235020 Brucella
U32810 Haemophilus
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AE001140 Escherich
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Belareva,A.V., Aleshin,V.V., Livshits,V.A., Tokhmakova,I.L. and
Zakataeva,N.P.
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Z15087 R.C
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT
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/db_xref="taxon:562"
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Bacherichia. Proteobacteria; gamma subdivision; Enterobacteriaceae; 1 (bases 1 to 11509)
Blattner, F. R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Length 840;
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of 400
 ; Score 618; DB 9; L; Pred. No. 9.7e-171; 0; Mismatches 0;
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Escherichia coli K12 MG1655
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AEOOO458.1 GI:2367299
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Escherichia coli K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="orf; Unknown"
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contains 1 REP sequence"
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/note="REP (repetitive extragenic palindromic) element;
contains 1 REP sequence"
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complement(4227. .4254)
                                                 .019. .1047

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="o610; 99 pct identical to 607 amino acids of RECQ_ECOLI SW: P15043 but has 3 additional N-ter
                                                                                                                                                                                                                                                                                                                                              /EC_number="3.6.1.-"
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complement(3654. .4070)
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Plunkett,G. III.

Bliect Submission

Submitted (13-071-1998) Laboratory of Genetics, University of Submission

Submitted (13-071-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. Coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG0301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently Getermined from E. Coli K12 strain MG1655. Predicted open reading frames were determined using Genemark software, Kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Allanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with Genet correlated with Genet genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the gatabase is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. Coli (http://www.genetics.wisc.edu). Annotation of the genome is of Monica (http://www.genetics.wisc.edu). *** The E. Coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated squence described in reference I. The unique numeric identifiers benefich and allower them to be searched for in Bntrez as gene agene agenes. This should allow them to be searched for in Bntrez as gene
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IGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQ
                               Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                     Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Blattner, F.R.
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                                                                                                                                                                                     /translation="MEOOOKDWETRENAFAAFTMGPLTDFWRQRDEAEFTGVDDIPVR
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5438. .5466

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5494. .5523
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99.8%;
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On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Misconsin-Madison. The entire sequence was independently determined from E. coli MG1665. Overlaps and conflicts with other sequence determinations are annotated. Reference [1] describes the original sequence determination of a 91408 bp sequence. References [2], [3], and [4] describe subsequent corrections and/or updates to that
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Rudd,K.E., Sofia,H.J., Koonin,E.V., Plunkett,G. 3rd, Lazar,S. and
Rouviere,P.E.
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Direct Submission
Direct Submission
Submitted (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu; Phone: 608-262-2534; Fax:
                                                                                                                                                                                                                                                                                    E. coli genomic sequence of the region from 84.5 to 86.5 minutes. M87049.
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Plunkett,G. III., Burland,V., Daniels,D.L. and Blattner,F.R. Analysis of the Escherichia coli genome. III. DNA sequence of region from 87.2 to 89.2 minutes
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
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Daniels,D.L., Plunkett,G. III., Burland,V. and Blattner,F.R. Analysis of the Escherichia coli genome: DNA sequence of the from 84.5 to 86.5 minutes
Science 257 (5071), 771-778 (1992)
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Blattner, F.R., Burland, V., Plunkett, G. III., Sofia, H.J. and
caacgtctggcgaagtggattgatggttttgccggggcgttatttgccggatttggcatt
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Analysis of the Escherichia coll genome. IV.
region from 89.2 to 92.8 minutes
Nucleic Acids Res. 21 (23), 5408-5417 (1993)
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Trends Biochem. Sci. 20 (1), 12-14 (1995)
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VTGKLNTFAHASVIHMDIDPAEMNKLRQAHVALQGDLNALLPALQQPLNQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MNGAQWVVHALRAQGVNTVFGYPGGAIMPVYDALYDGGVEHLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ilvG"
/note="CGSC No. 603; inactive in wild-type E. coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="acetohydroxy acid synthase II, large subunit"
/protein_id="AAA&67571.1"
                                                          /note="similar to Mg chelatase subunit of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="the mutation ilv02096 joins this ORF to ilvG, restoring function missing in wild-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgttgatgttatttctcaccgtcgccatggtgcacattgtggcgcttatgagccccggt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTALLRVISLVVISVVVIIIPPCGAALGRGKA"
3696. ,4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 91414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ilvGMEDA operon leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .341)"
                                                                                                                                                                                                                                                                                                                                                                                                                        3287. .3433
/note="predicted bend of 79 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3297. 3326
/note="promoter matrix score of 74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3336. .3737
/note="corresponds to V00289 (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3336. .3676
/note="corresponds to M11651 (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 96.1%; Score 594; DB 2; L Similarity 99.7%; Pred. No. 1.5e-163; 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="corresponds to M10313 (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(4677. .4678, "tatg")
                                                                                                                                              /function="unknown"
/protein_id="AAA67569.1"
                                                                                                                                                                                         /db_xref="GI:148173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:148175
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ilvg"
3696. .4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4675. .5340
/gene="o221"
                                                                                                                                                                                                                                                                                                                                                                                                      IHLOKLLT
                                                                                                                                                                                                                                                                                                                                                                                                                             misc_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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Matches 616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAHTSRHNEFSIGASASLWECMLNOWLGRLYQNQDAHTGLOFEA
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RLEWGPDFQQHEAGLIGADBYP ILTTSSABLAQOQIAMLNGCTWLPVSWARKKGGLHT
VVDSTTLSRPLYAIWLQNSDKNALIRDLLKINVLDEVY
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LDLGKREPVTEEEKLFVAVCRGEREPVTEAERVWSKYMTRIKRPKRFHTLSAVNRRLK
VLKTTPILTINKKGEMPFFYVSSFCRWMSKRSIAR"
DD861(EC17-221),DD864(EC27-149), DD865(EC21-76),
DD867(EC27-860). M13mpl9 or Janus vectors were used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            possible pssR gene"
                                                                                                                                                                                                                      'note="corresponds to V00349 (164. .500)"
                                                                                                                                                                         'note="corresponds to M37337 (1. .4900)"
                                                                                           . 200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253. .396
//orde="predicted bend of 81 degrees"
complement(266. .862)
/gene="f198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted bend of 77 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151. .1179
/note="promoter matrix score of 57"
1223. .1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="promoter matrix score of 63"
                                                                                       note="corresponds to K02846 (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     177. .205
/note="terminator-like sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLISGWDACIKIRMPIQAYSSKRELPNGSLW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="terminator-like sequence"
complement(1585. .3135)
/gene="f516"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="CGSC No. 18010;
                                                                                                                                 /note="clone EC15-116"
complement(1. .4899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(703. .1104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(266. .862)
/gene="f198"
                                                                                                                                                                                                                                                                                    1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'function="unknown"
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                                                                                                                                                                                                                                                              /gene="aspT"
/note="CGSC No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                   complement(1.
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                                              subcloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="trpT"
177. 205
                                                                                                                                                                                                                                                                                                                             'gene="aspT"
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/gene="o137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .223. .1636
'qene="o137"
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                                                                                                             .5863
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Location/Qualifiers 110592 (organism="Escherichia coli 0157:H7" /strain="EbL933" /strotype="0.015':H7" /db_xref="taxon:8334" /note="o-island #155; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655" complement(72836) /gene="5532" /gene="5532" /gene="5532" /gene="5532"	complement(7.2836) /gene="25332" /function="orf; Unknown function" /note="Residues 1 to 131 of 16 254 are 95.41 pct identical to residues 1 to 131 of 161 from Escherichia coli K-12 Strain MG1655: B3815" /codon_start==1 /transl_table=11 /protein_id="AA659008.1" /protein_id="AA659008.1" /protein_id="AA659008.1" /translation="MARRLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT /translation="MARRLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT /translation="MARRLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT /translation="MARRLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT /translation="MARRLIGKGMITLNLKRIFLALTLADMNSQGQVQMANNGGIYDESYAPLG /translation="MARRLIGKGMITLNLKRIFLALTLLDFTSTAPLGAVASKRINVE /translation="MARRLIGKGMITLNLKRIFLALTLLDFTSTAPLGAVASKRINVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSSYAPLGAVASKRINVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSSYAPLGAVAKLNVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSSYARAKLNVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSSYARAKLNVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSGQATNFYDFACTARAKLNVE /translation="MARRLIGKGMITLNLKRIRANGIYTRLADATLSGQATNFYDFACTARAKLNVE /translation="MARRLIGKGMITLNLKRIRA" /tr	12062156 /gene="corA" /note="2533" 12062156 /gene="corA" /note="corA" /function="transport; Transport of small molecules: /ations	/protein_id="AAGS9009.1" /db_xref="G1:12518687" /db_xref="G1:12518687" /translation="WLSABCFQUENNRLTRLEVEESQPLVNAVWIDLVEPDDDERLRVQS /translation="WLSABCFGDENNRLTRLEVEESQPLVNAVWIDLVEPDDDERLRVQS /translation="WLSABCFEDDGLHIHSFFFEDAEDHAGNSTVAFTIROGRLF TLARRELPAFNEYKRMARSQSWYDGNNYELLDJGFFFTEDAEDERNIYSDLEQLSR VIMEGHQGDEYDEALSTLAELEDIGMKVRCLLMJGTRALNFLVRKARLGGGQLEQARE VIMEGHQGDEYDEALSTLAELEDIGMKVRCLLMJGARLNFLVRKARLGGGQLEQARE ILRDIESLLEHNESLEOKVNFLMQAAMGFINIEQNRIIKIFSVVSVVFLPPTLVASSY GMNFEFMPELKWSFGYPGAIIFMILAGLAPYLYFKRKNWL" 2157.	/ LIGHSCALCE_II. // Protein_laisCALCE_II. // Protein_lais_ACS9010.1" // Ab_xref="G1:12518688" // Ab_xref="G1:12518688" // LICELELCCIVILWTLRPVQILYTYSDAGNSVFLVV // LICELELCEDSSHITWYLLEPEDS TO THE TRANSPORT TRIVENT TREEPTEDLY CEPTIKENDENT TRIVENT TRIVENT TRICEPTEDLY CEPTIKENDENT TRIVENT TRIVENT TRICEPTEDLY COMPLEMENT (26863534) // Gene="Z5335" // Gene="Z5335" // Complement(26863534) // Gene="Z5335" // Complement(26863534)
FEATURES SOURCE misc_feature gene	CDS	gene CDS	misc_feature gene CDS	gene
60863 ATGTTGATGTTATTCTCACCGTCGCCATGGTGCACATTGTGGCGCTTATGAGCCCCGGT 61 cccgatttcttttttgtctctcagaccgctgtcagtcgttcccgtaaagaagcgatgatg 61 11111111111111111111111111111111111	61043 241 61102 301 61162 361 61221	421 ggtgataacqttgggataacgtggggatattttggggataacgtggggatattttgggtgataacgtggggatacgtlgggataacgtgggataacgtgggataacgtgggataacgtgggataacgtgggataacgtgggataacgtgggggggg	Db 61461 CATTTCATTATTCGGG 61478 RESULT 4 AE005613 10592 bp DNA BCT 25-JAN-2001 LOCUS ACCESSION AE005613.1 G1:12518685 ACCESSION AE005613.1 G1:12518685 REFWORDS Escherichia coli 0157:H7. ORGANISM Escherichia coli 0157:H7. Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae; BSCHINTION Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae; BSCHINTION BACTERIA. BSCHINTION BACTERIA. BSCHINTION AE005613.1 G1:12518685 AUTHORS PERENCE 1 (bases 1 to 10592) AUTHORS POSSEA1, G., Harkett, G. III, Burland, V., Mau, B., Glasner, J.D., POSSEA1, G., Harket, J. Kirkpatrick, H.A., POSSEA1, G., Harket, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,	Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R. TITLE Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 JOURNAL Nature 409 (6819), 529-533 (2001) REFERENCE 2 (bases 1 to 10592) AUTHORS Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatitick, H.A., Pose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatitick, H.A., Grotbeck, E.J., Davis, N.W., Lin, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Walch, R.A. and Blattner, F.R. TITLE Direct Submission JOURNAL Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

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/function="orf; Unknown function"
//note="Residues 1 to 161 of 161 are 100.00 pct identical
to residues 1 to 161 of 161 from Escherichia coli K-12
strain MG1655: B3820"
//cadol_start=1
//transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggtgataacgttggcactaccgcgcgctggggcatttttgcgctgatcattgtcgaaacg 480
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                                                                                                                                                                                                                                                                                                                 /function="enzyme; Central intermediary metabolism:
Phosphorus compounds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catttgattatcgaaaaatggcctggctgcatacgctgattatggtgggcggtggcctg
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10592;
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 592.4; DB 1;
Pred. No. 3.9e-163;
0; Mismatches 16;
   complement(5780. .6265)
                                                                                                                                                                                                                                   6412. .7281
/gene="pldA"
/note="Z5342"
                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                   /gene="yigI"
                                                                                                                                                                                                                                                                                  6412. .7281
/gene="pldA"
                                                                                                                                                                                                                                                                                                                                                                                                                          95.9%;
ilarity 97.4%;
Conservative
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residues 8 to 299 of 300 from Escherichia coli K-12 Strain
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Consensus quality: 253950 bases at least Q40
Consensus quality: 253950 bases at least Q30
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Consensus quality: 258916 bases at least Q30
Consensus quality: 258916 bases at least Q30
Estimated insert size: 273689; sum-of-contigs estimation
Quality coverage: 9.54 in Q20 bases; agarose-fp estimation
Quality coverage: 7.53 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 27958)
DOE Joint Genome Institute.
                                      AC073768 279589 bp DNA HTG 29-JUN-2000
Mus musculus clone RP23-359N18, WORKING DRAFT SEQUENCE, 60
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1009: contig of 1009 bp in length 1109: gap of unknown length 2132: contig of 1023 bp in length 3257: contig of 1025 bp in length 3257: contig of 1025 bp in length 3357: gap of unknown length 4550: contig of 1193 bp in length
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Center Project Name: 1875058
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Direct Submission
Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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----Summary Statistics
Estimated insert size: 212936; sum-of-contigs estimation
Estimated insert size: 157000; pulse field gel estimation
Quality coverage: 4.20x in 020 bases; pulse field gel estimation
Quality coverage: 3.10x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
ACU20970 212936 bp DNA HTG 10-FEB-2000
Mus musculus clone RP23-252M21, WORKING DRAFT SEQUENCE, 144
unordered pieces.
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Mammalia; Eutheria; Rodentia;
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68603 c 67231 g 68544 t 5957 others
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gap of unknown length
contig of 29530 bp in length.
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of 15113 bp in length
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of 27875 bp in length
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Pred. No. 1.1e-152;
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of 26817 bp in
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of 4448
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/db_xref="taxon:10090"
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18309 19519 20711 21933 23607 25329 26650 27850 29136	30701 31878 33066 34268 35475 36651 37860 39073 40407	42865 44201 46088 49519 50911 52421 53614 55005 56301 57506	60408 61633 62881 64221 65421
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/crideroc=not_experimental
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ARQQLSALNGCSWLPVNWANEKGGLHTVADSATLSRPLYAIWLQNSDKYSLICDLLKT
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Agene="SYMOI.99"

complement(1506. .2354)
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/note="83# identity with E. coli hypothetical protein
(YIFA) (SP:P22788) and 95% identity with amino acids 1-80
of E. coli possible regulatory protein (PSSR) (SP:P27826)"
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LDLGKREPVTEEEKLFVAVCRGEREPVTDAERVWSKYMTRIKRPKRFHTLSGGKPQVE
                                                                                                                Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs CALIMDRR (SAL2Derg, S., DeLcher, A., Kasif, A. and White, O. (1998) NAR 26,544-548), and GeneMark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,1107-1115.
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similarity to Pfam family
subunit ChlI), score=351.8,
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such as compressions and repeats; all regions were covered sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                   /organism="Salmonella typhimurium LT2"
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/transl_table=11
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(YIFB) (SP:P22787); contains s
PF01078 (Magnesium chelatase,
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1072. 1191
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                                                                                                                                                                                                                                        Location/Qualifiers
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1329. .1401
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2461. .2799
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Submitted (09-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174321 CCCGATTC-TTTTTGTCTCTCAGACCGCTGTCAGTCGTTCCGTAAAGAAGCGATGAT- 174378
                                                                                                                                                                       174497 TATCTCTGCTGGATGGGTTACCAGATGCTA-GTGGTGCACTGAAAAAAAAGGGCGGTTTCT 174555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 174615 ACCAATCTCG-TAATCCGAAAGCGATATCTACTTTGGCTCGGTGTTCTCATGTTTGTC 174673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctggcgtggtttaccgtcgttgccagcctgtttgccctgccgcaaatgcgccgtggttat 540
  cccgatttcttttttgtctctcagaccgctgtcagtcgttcccgtaaagaagcgatgatg
                                                                                     ggcgtgctggggcattacctgcggcgtaatggtttggggctgggattgcgctggcttggcctg
                                                                                                                                                                                                                                                            tatetetgetggatgggttaccagatgctacgtggtgcactgaaaaaaagaggcggtttet
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St. Louis, MO 63110, USA
e-mail: sclifton@watson.wustl.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 96086)
Washington University Genome Sequencing Center.
The Salmonella typhimurium Genome Sequencing Project
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STYSTMD1 96086 bp DNA
Salmonella typhimurium fragment STMD1.
AF233324
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4934. 6580

/gene="11vG_1"

4934. 6580

/gene="11vG_1"

/gene="11vG_1"

/codon_start=1

/transl_table=11

/product="92% identity with B. coli acetolactate synthase

II (ILVG) (SF:P00892) ; contains similarity to Pfam

family PF00205 (Thiamine pyrophosphate enzymes),

score=925. E. 1.3e-295, N=1"

/db_xref="G1:6960293".
                                                                                PGTGKTMLASRLSGILPPLSNEEALESAAILSLVNADTVQKRWQDPRTSPHRASLT
AWVGGGAIPAPGEISLAHNGILFLDBLPEFERRTLDALREPTESGUPHLSRPRAKITY
PARFOLIAAWNESPTGHYGNHNRCTPEPGILSVLRLSGFFLDRFDLSLEIPLPPPGI
LSGHASKGESSATVKKVIDAHROYRRQKKLNARLEGFREIGKTCVLHHDDARWLEDT
LVHLGLSIRAWQRLLKVARTIADIELADQISRQHLQBAVSYRAIDRLLIHLQKLLA"
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FTAYTOMPYVTCTLKGIGAVBADYPYLTLAMIGARGRIGTRAANFAYOEDDLI.JAVGAREDDR
VTGKILMTFAPRASVIHMDIDPABMYLILLAGGDINSI.LPALQQPIKIDDRA
AELRAEHAWRYDHPGETIYAPILLKQLSERKPADSVYTTDVGQHQMWSAQHMTYTRPE
NTTSSGGTTWAFFGLPAAVGAQVARRYNDYTOLGSTGSTGSTGSTGAGNAVQELFVERKQLPKI
VLLDNQRRGWYRQWQQLFFQBRYSETTLTDNPDFLMLASAFGIPGQHTTRKDQVEAAL
DYMLASEGFYLLHVSIDELENVWPLVPPGASNSEMLEKLS"
                          AYELVGELALTGALRGYPGAISSATEAIRAGRNIIVATENAAEVGLISKEGCFIADHL
OTVCAFLEGKHALERPLAQDMASPTATADLRDVIGQEQGKRGLEITAAGGHNILLIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNGAQWVVHALRAQGVKTVFGYPGGAIMPVYDALYDGGVEHLLC
RHEQGAAMAAIGYARSTGKTGVCIATSGPGATNLITGLADALLDSVPVVAITGQVSAP
FIGTDAFQEVDVLGLSLACTKHSFLVQSLEELPRIMAEAFEVANAGRPGPVLVDIPKD
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NIELIYASPRSYDLLFSQLSKLYDVAHVAICQSAATSQQIRA"
6858. 7787
/gene="ilve"
6858. 7787
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SHKGPVVFRHREHWQRLRDSAKIYRFPVSQSIDELMEACRDVIRKNNLTSAYIRPLVF
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AGGNYLSSLLVGSEARRHGYQEGIALDVNGY ISEGAGENLFEVKDGVLFTPPFTSSAL
PGITRDAIIKLAKELGIEVREQVLSRESLYLADEVFMSGTAAEITPVRSVDGIQVGEG
ARDRVRSAIINSGYEFPAKKITINLAPADLPKEGGRYDLPIAVALLAASEQLTASNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="100% identity to E. coli ilvGMEDA operon leader peptide (ILVL) (SP:03060)"
/protein_id="AAR33486.1"
/db_xref="GI:6960296"
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transaminase (ILVE) (SP:P15168)"
/protein_id="AAR33481.1"
/db_xref="G1:6960291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTALLRVISLVVISVVVIIIPPCGAALGRGKA"
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/transl_table=11
/product="93% identity with E. of pluy) (SP:P13048)"
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                                                                                                                                                                                                                                                                                                  4696. .4794
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/note="STMD1.90"
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/transl_table=11
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4696
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/gene="ilvM"
6580. .6840
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gene

CDS

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CDS

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CDS

RCGPVTKRIQQAFFGLFTGETEDKWGWLDPVNS"

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(SP:P40810); contains similarity to Pfam family PF00920
(Dehydratase family), score=1023.9, E=3.5e-304, N=1"
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QDCRWDSLDDDRAAGCIRSLEYAYSKDGGLAVLYGNFAENGCIVKTAGYDDSILKFTG
PAKYYESQDDAVEALIGGKYVEGDVYVIRYEGPKGPEMQEMIYPTSFLKSMGLGKAC
ALITDGRFSGGTSGLSIGHVSPEAASGGTIALIEDGDTIAIDIPNRSIQLQLSEAEIA
ARREAQEARGDKAWTPKNRQRQVSFALRAYASLATSADKGAVRDKSKLGG"
9801. .11345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggcgtgctgggcattacctgcggcgtaatggtttgggctgggattgcgctgcttggcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggtgataacgttggcactaccgcgcgctggggcatttttgcgctgatcattgtcgaaacg
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Pred. No. 4.7e-119;
0; Mismatches 109;
                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                      /note="STMD1.88"
7948. .9798
/gene="ilvD"
7948. .9798
/gene="ilvD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.6%;
llarity 82.3%;
Conservative
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es 508;
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ACOUNTIES 266294 Up. DMA. HTG 16-FEB-2000 ACOUNTIES THESE PRESED. ACOUNTIES THESE PRESED. ACOUNTIES THESE PRESED. ACOUNTIES THESE PRESED. ACOUNTIES THE ACOU	13911:	14819: contig	(0 15571; contig of 752 bp in Length gap of unknown length	15872: contig	3 16608: contig	gap or 16851: contig	gap of	gap of	18057: contig	18704: contig	gap oi 19414: contig	gap of	gap of	21010: contig	21258: contig	gap ol 22363: contic		gap of	24853: contig	25795: contic	gap or 27027: contig	gap of 27729: contic	gap of	28722:	29714: contiquent	30858: conti	9ap Oi 31397: contig	gap of 31671: contig	gap of 32959: contig	gap of		34648: COULLY gap of	gap of gap of	35776: contig gap of	35903:	36602: contig	gap of 37110: contig	gap of	gap of	38/30: contig gap of	39790: contig qap of	40327: contig	gap of unknown length
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שו פוט שו פוט שו בעום בעום בעום בעום בעום בעום בעום בעו		AC020885 268294 bp DNA HTG	Mus musculus clone RP23-464I1, LOW-PASS SEQUENCE AC020885		house	Mus musculus Eukaryota; Metazoa; Chordata; Craniata	Mammalia; Eutheria; Rodentia; Sciurogn	DOE Joint		CE 2 (bases 1 to 268294)	DOE Joint Genome Institute. Direct Submission	JOURNAL Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint	Genomie Institute, 2000 Mitumeil Diive, Mainut Creek, CA 94390, USA On Feb 16, 2000 this sequence version replaced gi:6686423.	* NOTE: This record contains 183 individual * commenciate that have not been accoming into	* contigs, Runs of N are used to separate the reads	* and the order in White Liety appear is completely * arbitrary. Low-pass sequence sampling is useful for	identifying clones that may be gene overlap relationships among clones	However, it should not be assumed	* Will be sequenced to completion. In the event that * the record is updated, the accession number will *	* be preserved.	gap of un	1615: contig of qap of un	2405: contig of 790 k	gap of unknown 3234: contig of 829 h	gap of un 3533: contig of	gap of un)	gap of unknown	5401: contig of 934 k gap of unknown	6154: contig of 753 h	6629: contig of	7176: contig of	yap or una 7824: contig of	8656: contig of 832 h	gap of unknown 8865: contig of 209 k	gap of unknown 9544. Contid of 679 b	gap of unknown	10280: contig of 736 b gap of unknown	10975: contig of 695 b	11742: contig of 767	gap or unknown 12178: contig of 436	gap of unknown lass 12887: contig of 709 bp	gap of unknown l	1350/: contig gap of

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University (bases) 1 to 290452)
Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R., Ishihkhes,I.P., Shim,C., Decker,J., Thomas,B., Perera,A., Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission. G12-Aug-2000) Department of Molecular Genetics, Albert Submitted (23-Aug-2000) Department of Molecular Genetics, Albert Binstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
On Aug 30, 2000 this sequence version replaced gi:9885883.
Albert Einstein College of Medicine Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 290452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC079167 290452 bp DNA HTG 30-AUG-2000 Mus musculus chromosome 6 clone RP23-226D23 strain C57BL6/J, *** SEQUENCING IN PROGRESS ***, 196 unordered pieces.
* NOTE: This is a 'working draft' sequence. It currently consists of 196 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                    ccgcgcgctggggcattttgcgctgatcattgtcgaaacgctggcgtggtttaccgtcg
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High Throughput Mouse Sequencing
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Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 196511 at least Q20
*Consensus quality: 172308 at least Q30
*Consensus quality: 138790 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 286552 - sum-of-contigs
Quality coverage: agarose-FP - N/A
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Quality coverage: 3.3x sum-of-contigs
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HTG; HTGS_PHASE1.
house mouse.
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KIGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFN
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                                                                                        Db 104019 GTAAAGATINNNNNNNNNNNNNNNNNNNNNTACGTGGTGCACTGAAAAAAGA-GCGGTTTC 104077
                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                   240 gtatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaagaggcggtttc 299
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E.coli recQ gene complete cds, and pldA gene, 3' end.
M30198
M30198.1 GI:147557
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Irino, N., Nakayama, K. and Nakayama, H.
The recQ gene of Escherichia coli K12: Primary structure evidence for SOS regulation
MO1. Gen. Genet. 205, 298-304 (1986)
87115164
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                      Length 290452;
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Pred. No. 1.4e-88;
0; Mismatches 25;

    2695
/organism="Escherichia coli"
/strain="K-12"

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REQOLEVWIGCRTGGIRLIYIATAPERLALDNTLEHLAHWNPVLLAVDEAHCISGWGHDF
REQOLEVWIGCRTGGIRLIYIATAPERLALDNTEHLAHWNPVLLAVDEAHCISGWGHDF
REDAMLFYDEADMAAVLRYCEGREKFOGOLODIERHKLANAMGAAALGSKGISAAAXHAGLENNV
RADVQEKFORDDLQIVVAYVARGMGINGNEHKLANAMGAREAALGSKGISAAAXHAGE
BABAALFYDFADMAAWLRKLEERFQGGLODIERHKLANAMGAREAAGYCRELVILNYFG
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DYGHDKLKYTGMGRDKSHEHWYDGDIHLGLYVUNIAGARSALQITEAARPVLAESS
LQLANPRIVALKPRAMQKSRGGNYDRKLEREKIRKLRKSIADBENVPPYVVFNDATLIE
MAEQMPITASEMLSYNGVGMRKLERFGKRFFALIRKLRKSIADBENVPPYVVFNDATLIE
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DOE Joint Genome Institute.
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Mus musculus clone RG-MBAC_40H2, LOW-PASS SEQUENCE SAMPLING.
ACO20833
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Pred. No. 5.1e-76;
0; Mismatches 2;
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HTG; HTGS_PHASE0.
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Best Local Similarity 98.8%;
Matches 319; Conservative
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20213	18/16 19494	17939	17162	16427	15739	14870	14027	13879	13131	12678	11696	10891	10273	6496	9059	8254	7567	6854	6455	5585	5297	4767	3646	2954	2421	1813	1050	297	

22941 23943: contig of 562 bp 22941 23943: contig of unknown and appeal of unknown and and and and and and and and and an	* *	157	237	contig gap of	808 bp in l known length	ength
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* 53729 56784: contig of 3056 bp * 56785 59220: contig of 2436 bp * 56785 59220: contig of 2436 bp * 59221 62274: contig of 3054 bp Location/Qualifiers	k * ·	166	3728	o <u>-</u> j	known tength 2067 bp in 1	ength
* 56785 59220: contig of 2436 bp i * 59221 62274: contig of 3054 bp i Location/Qualifiers 162774	* * *	372	6784	0 🗄 0	Known length 3056 bp in l	ength
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rce 162274		9221	62274	gap o conti	3054 bp in 1	ength.
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DOE Joint Genome Institute.
Direct Submission
Submitted (10-JAN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 298166)
                                                                                                                                                                                                                                        Consensus quality: 189570 bases at least Q40
Consensus quality: 207567 bases at least Q30
Consensus quality: 21722 bases at least Q30
Estimated insert size: 231000; agarose-fp estimation
Estimated insert size: 290766; sum-of-contigs estimation
Quality coverage: 8.11 in Q20 bases; agarose-fp estimation

Quality coverage: 6.44 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a work of the processive consists of 75 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                  357 actgaccaatctcgctaatccgaaagcgattatctactttggctcggtgttctcattgtt 416
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                                                                                                                                       Length 62274;
                                                         341 others
                                                                                                                                   Query Match 39.3%; Score 242.8; DB 66; Length Best Local Similarity 95.4%; Pred. No. 2.4e-60; Matches 250; Conservative 0; Mismatches 12; Indels
/organism="Mus musculus"
/db_xref="haxon:10090"
/clone="RG-MBAC_40H2"
| 13547 c 13251 g 18170 t
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Sequencing of Human Chromosome 16
Unpublished
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Center Project Name: 0
Center clone name: RPCI-11_358F6
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SEQUENCE, 75 unordered pieces
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AC087563.1 GI:12061429
HTG; HTGS_PHASE1; HTGS_DRAFT.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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DOE Joint Genome Institute.
Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5649 145748: gap of unknown length
5749 164949: contig of 19201 bp in length
4950 165049: gap of unknown length
5050 198403: contig of 33354 bp in length
8504 243378: contig of 44875 bp in length
8504 243378: contig of 44875 bp in length
3379 243478: gap of unknown length
10cation/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/chromosome="16"
/clone="RP11-358F6"
/clone="RP11-358F6"
                                                                                                                                                                                                                                                                   Query Match 21.5%; Score 132.8; DB 78; Best Local Similarity 60.9%; Pred. No. 5.6e-28; Matches 266; Conservative 0; Mismatches 168;
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DOE Joint Genome Institute
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 265383)
DOE Joint Genome Institute.
Sequencing of Mouse
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mus musculus clone RP23-333M14, LOW-PASS SEQUENCE SAMPLING.
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                                                                                        * NOTE: This record contains 8 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
be preserved.
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Pred. No. 2.4e-24;
0; Mismatches 10; Indels 3
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gap of unknown length
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4256: contig of 1204 bp in length
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gap of unknown length
1566: contig of 730 bp in length
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                                                                 Web site: http://www.jgi.doe.gov
                    -----Genome Center
Center: Joint Genome Institute
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Direct Submission
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
On Feb 16, 2000 this sequence version replaced gi:6686434.
* NOTE: This record contains 244 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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gap of unknown length
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Pasteurella multocida
Bacterrai, Proteobacteria; gamma subdivision; Pasteurellaceae;
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1 (bases 1 to 10184)
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Pasteurella multocida PM70 section 77 of 204 of the complete
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                                                                                            Complete nucleotide sequence of an avian isolate of Pasteurella
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                          Zhang,Q., Li,L., Paustian,M.L., Whittam,T.S. and
                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pasteurella multocida"
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/codon_start=1
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1. .10184
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complement(7842. .8504)
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/trans1_table=11
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	E. coli L-threonin	Escherichia coli y	Stealth virus nuci	Escherichia coli y	Gene encoding a su	A. vitis hypersens	A. vitis hypersens	Human ORFX ORF1040	Photorhabdus lumin	Neisseria gonorrhe	Stealth virus nucl
	ID	A48443	A52688	X84330	A52689	A10594	A61501	A61502	C75485	T68841	253939	X84332
	DB	21	21	20	21	21	21	21	21	18	21	20
	Query Match Length DB	840	672	8387	639	10732	1668	1668	565	3288	2178	5059
dР	Query Match	100.0	8.9	5.9	5.6	5.6	5.4	5.4	5.2	5.2	5.1	5.1
	Score	618	54.8	36.2	34.8	34.8	33.4	33.4	32.4	32	31.6	31.6
	ult No.	-	7	3	4	Ŋ	9	7	80	6	10	11
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Modified carboxyl Human adenosine Al Mycobacterium tube BCG deletion region Neisseria meningit Noisseria meningit Nochacterium tube Human thiazide-sen Rhizobium species Noisseria meningit Noisseria meningit Noisseria meningit Noisseria meningit Pinus radiata cell Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_1 encod Clone if87_2 encoding a maxis encoding a maxi		Tokhmakova IL;
111 Q06352 20 X53491 21 A89440 21 A89440 21 Z5426 21 Z5426 21 A81472 21 A81489 12 V29932 21 A81489 12 V29932 21 A81473 20 V72577 20 V72577 20 V72577 21 A81487 22 V30459 23 X80671 21 A93323 21 A93323 21 A93323 21 A73346 21 A73346 21 A73366 21 A590077 22 C30077 23 C30077 20 X5040	ALIGNMENTS; DNA; 840 BP. irst entry) nine resistance gene, rhtC. istance; L-threonine synthesis; rhtC; valine; L-leucine; ds. Location/Qualifiers 187.807 /*tag= a /product= "RhtC" 199EP-0125406. TO KK.	NP, Aleshin VV, Belareva AV,
5.0 114955 5.0 114955 5.0 168836 5.0 168836 5.0 105836 6.5 5.0 175225 6.5 5.0 175225 6.5 5.0 175225 6.5 6.0 175225 7.0 17522 7.0	(f (f hreo. res e; L col 1.	VA, Zakataeva 0-414602/36. Y99598.
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 A48443 ID A48443 stan XX AC A48443; XX DT 08-SEP-2000 XX C-threonine XW L-threonine XW L-threonine XX C-threonine XX	Livshi WPI; 2 P-PSDE

BP

672

standard; DNA;

A52688

(first entry)

03-JAN-2001

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           Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced Rhtc protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                        The present sequence is the L-threonine resistance gene, rhtC, from Eschericha coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding will-threonine at a concentration at which the corresponding will-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
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                                                                                                                                                                                                                                                                                                         Length 840;
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                                                                                                                                                                                                                                                                                                       Score 618; DB 21;
Pred. No. 4.1e-193;
0; Mismatches 0;
                                                                    English
                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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Best Local Similarity 100.
Matches 618; Conservative
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The present sequence is the yahN gene (an excretion protein gene) of sechericals coll. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                  production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
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Pred. No. 4.5e-08;
0; Mismatches 307;
                                                                                                                                                                                                                                                                                                                                                             Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 17-18; 29pp; English.
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1..672
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                                                                                                                                                                                               "Yahn
                                                                                              amino acid
                                                                                                           excretion protein;
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99RU-0104431.
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                                                                      Escherichia coli yahn gene
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P-PSDB; B01786.
                                                                                               yahN gene;
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Tokhmakova IL;
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RESULT A52688

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specification, and are included to maintain the
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                                   gtgggcgcagtttcctgaaaggtttactgaccaatctcgctaatccgaaagcgattatct
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8118
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This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA whith a molecular probe that method is used to detect stealth virus in a biological product, food or in the environment. The method is also used to evaluate agents for their chibitory or stimulatory effects on stealth virus replication and to cherential capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8286 NAYNKMDHGVINTTHVGVNTHCHAAGVVHGGDHHYWASYGKNAYTKNDWTKYNNAYTKND 8227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8346 SNKHTSYAAMVKGCWNATKYNRYTKKSANKGHNATKYNRYTKKSANKGHHYWVTASTRYA 8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acgiggigacactgaaaaaaagaggggtttctgcacctgcgccacaggtcgagctggcgaa 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 ggtttggggctgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcctggct 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. colli yeaS gene; amino acid production; excretion protein gene;
amino acid excretion protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : : | : | : | : | : | : | HANAYTKNDWNANDTYCTYTATHTDKTKYNTVGHNNNNCDMKNYSABWRNTDWGAATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 gcatacgctgattatggtgggcggtggcctgtatctctgctggatgggttaccagatgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagtggggggagtttcctgaaaggtttactgaccaatctcgctaatccgaaagcgattat
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8387;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8387 BP; 1807 A; 2320 C; 2218 G; 1844 T; 198 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 36.2; DB 20; 23.5%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.2;
87; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggcatttttgcgctgatcattgtcga 476
                                                      Claim 19; Page 61-64; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                 Novel strains of stealth virus
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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(MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO.
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                                                                                                                                                                                                                                                                  The present sequence is the yeas gene (an excretion protein gene) of schericals coll: The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alamine, valine, histidiane, isolaucine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                               Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                      318 cgagctggcgaaaagtgggcgcagtttcctgaaaggtttactgaccaatctcgctaatcc 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 gaaagccattttgttctatgtgtcgtttttcgtacagtttatcgatgttaatgccccaca 443
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Troshin PV;
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                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 34.8; DB 21; Length 639; 50.6%; Pred. No. 0.16; Live 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taccgcgcgctggggcattttgcgctgatcattgtcgaaacgctg 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 tacgggaatttcattcttattctggcggcgacgctggaactggtg 489
                                                                                                                                  Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                            Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding a subunit of cellulose synthase.
                                                                                                                                  Nakanishi K,
                                                                                                                                                                                                                                               Disclosure; Page 19-20; 29pp; English.
                                                       99EP-0125263.
                                                                           98RU-0124016.
99RU-0104431.
                                                                                                                                  Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4/c
A10594 standard; DNA; 10732
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.6
nes 84; Conservative
                                                                                                           (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                 WPI; 2000-414802/36.
P-PSDB; B01787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellulose synthase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2000060568-A.
                                                                                                                               Livshits VA,
Tokhmakova IL;
          EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1998;
                                                    17-DEC-1999;
                                                                                      09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1998;
                                                                           30-DEC-1998;
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                               05-JUL-2000
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Matches
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of
                                                                                                                                                                          This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9728 AYDACYDAYDANCYSSDSTYTBYCSRRCCCYYDAYSCSRYDARCYDACYSYSNSTCYDAT 9669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : :: |:: :: | |:: |: | 39668 BTTSRYSTTYSYSNCYDATTSRCTBYSTBTBTTSRCAKCTBDSTSTARNSTSTYSTTRC 9609
                                                               gene encoding a cellulose synthetic equipment – for the improvement the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 gettatgageeceggteeegatttettttttgteteteagaeegetgteagtegtteeeg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 taaagaaagcgatgatggggggtgctggggcattacctgcggcgtaatggtttggggctgggat 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 tgcgctgcttggcctgcatttgattatcgaaaaatggcctggctgcatacgctgattat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9608 TBYSSRSRGYSYCSRSRCYSCYTDSDSTCYSTTYSTTYAYSCTTSRGYSYD 9556
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 10732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 ggtgggcggtggcctgtatctctgctggatgggttaccagatgctacgtggtg 277
                                                                                                                                                                                                                                                                                                                                     Seguence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.6%; Score 34.8; DB 21; Best Local Similarity 15.9%; Pred. No. 0.65; Matches 37; Conservative 101; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376567/32.
P-PSDB; B11630, B11631, B11632, B11633, B11634.
                                                                                                                                 Claim 2; Page 14-21; 32pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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WPI; 2000-342371/30
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New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of

WPI; 2000-376567/32. P-PSDB; B11635, B11636, B11637, B11638.

Herlache TC, Zhang

Burr TJ,

(CORR) CORNELL RES FOUND INC

99WO-US26079. 98US-0107387.

05-NOV-1999; 06-NOV-1998;

18-MAY-2000

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Grobacterium vitis hypersensitivity response (HR) elicitor proteins adjoined with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or vituses; and to enhance growth, e.g., to increase yield or to provide carlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of Day that encodes A. vitis HR elicitor proteins. The proteins of the provide same effects can be produced by producing transgenic plants or seeds by a vitis HR elicitor proteins. Ose of a vitis HR elicitor proteins. Ose of a vitis the provide of a vitis the proteins of a vitis the provide of a vitis the proteins. On nucleic acids encoding them, may allow and a vities the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provide of the provi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irol of previously untreatable diseases; provide systemic treatment; eliminate the need for biological control agents or polluting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tggcgcttatgagccccggtcccgatttcttttttgtctctcagaccgctgtcagtcgtt 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    677 TGGCCGTTCTCAGCCCCGGCGCGGATTTTGCCATGGTGTCGCGCAATAGTTTTCTTTATG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 cccgtaaagaagcgatgatgggcgtgctgggcattacctgcggcgtaatggtttgggctg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      617 GCCGCAAATCCGGGCTGGCGGCCTCGATGGGCATTGCCATTGCCTGCTGGTTTCATGTGA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 ggattgcgctgcttggcctgcatttgattatcgaaaaaatggcctggctgcatacgctga 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557 TCTATGCCATGTTCGGCATTGCGATCATCCAGCATATTTTCCCCAATATTCTGGATATCA 498
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                            New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response ellcitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant; ds.
                                                                                                                                                                                                          Sequences A61501-A61524 represent nucleotide sequences encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.4; DB 21;
Pred. No. 0.75;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttatggtgggcggtggcctgtatctctgctggatgggtt 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rcaaatrcercecececerarcreercrateceeerr 459
                                                                                                                                              Claim 7; Page 82; 157pp; English.
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                                                                                        hypersensitive response
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Suppose that is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and cocurs when a pathogenic organism interacts with a nonhost plant is associated with the active defence of plants against many pathogens, and cocurs when a pathogenic organism interacts with a nonhost plant (1.e. one in which intracellular bacterial growth and disease development do not occur. Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fund; bacteria cor viruses; and to enhance growth, es, to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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0; Mismatches 116;
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ID C75485 standard; cDNA; 565
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Matches 103; Conserv
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vulnerary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidalamatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; encurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                  Human ORFX ORF1040 polynucleotide sequence SEQ ID NO:2079
08-FEB-2001 (first entry)
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Homo sapiens

WO200058473-A2

05-0CT-2000

31-MAR-2000; 2000WO-US08621.

99US-0127607 31-MAR-1999;

990S-0127636. 990S-0127728. 20000S-0540763. 02-APR-1999; 05-APR-1999; 30-MAR-2000;

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57. P-PSDB; B41276.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 1566; 5507pp; English.

cytyto to C77606 encode the proteins given in B40237 to B43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dernatiological; immunosuppressive; antidiabetic; hypotensive; antiviral; antifungal; antithreumatic; antithryoid; and antianaemic. The sequences can be used for determining the presence of or predisposition or preventing or treating pathological conditions associated with an organizated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors: The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative cused to treat cancers, proliferative disorders, neurodegenerative disorders storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders and section and antide and a disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 565 BP; 122 A; 169 C; 148 G; 126 T; 0 other;

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                          Gaps
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0
5.2%; Score 32.4; DB 21; Length 565; 50.6%; Pred. No. 0.95;
                          Indels
                       16;
                           0; Mismatches
                            78; Conservative
  Query Match
Best Local Similarity
Matches 78; Conserv
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This genomic DNA sequence encodes insecticidal toxin protein Teah (see W17888-89) of Photorhabdus luminescens, a component of a toxin protein complex. Claimed toxins of P. luminescens (see W17871, W17884-89, W17899-900, W18301-06) can be produced by recombinant DNA methods and applied to, or genetically engineered into, insect larvae food and plants for insect control. The photorhabdus toxins are particularly effective against Southern corn rootworm, Colorado potato beetle, Western corn rootworm, meal worm, boll weevil and turf grub (Coleoptera), beet armyworm, black cutworm, cabbage looper, codling moth, corn earnyworm, black borer, tobacco hornworm and tobacco budworm (Lepidoptera), and are also active against insects of the orders Hymenoptera, Diptera, Dictyoptera, Acarina and Homoptera. (All claimed).
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caggicgagctggcgaaaagigggcgcagittccigaaaggittacigaccaaictcgci 372
                                                                  97
                                                                                                                                                                           156 CAGAICGAITHGIGGGAAATHGGCCAGGGCCTTTCAACGCGCTTGAGAGTGATCTCGTT
                                                                                                                                        373 aatoogaaagogattatotactttggotoggtgttctoattgtttgtoggtgataaogtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insecticide; insect; toxin; pest control; biological control; photorhabdus luminescens; TcaA; Southern corn rootworm; Colorado potato beetle; Western corn rootworm; meal worm; boll weavil; turf grub; Coleoptera; beet armyworm; black cutworm; cabbage looper; codling moth; corn earworm; European corn borer; tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera; Diptera, Dictyoptera; Acarina; Homoptera; ds.
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Orr GL;
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Guo L, Hey TD, Merlo DJ,
Rocheleau TA, Schoonover
                                                                                                                                                                                                                                                                             433 ggcactaccgcgcgctggggcattttgcgctga 466
                                                                                                                                                                                                                                                                                                                                               36 TTCACCTTCACGATCAGGGTCGGTTGCGAGGTAA 3
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95US-0007255.
96US-0608423.
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Petell J, Roberts JL,
Strickland JA;
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P-PSDB; W17888-89.
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28-FEB-1996;
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             313
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misc_difference
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                                                                                                                                                                    Query Match
Best Local Si
Matches 55;
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                                                                                               2728 TGGCATTGTCATGGCTAAACAGGGTTTGATTATCATGCCAGTAGTTTGCCAATGTAAAAG 2669
                                                                                                                                              2608 TCTTAATGCCGAAACCGGCGCTTAGCGCCCGCAGCACTTTCTGCTGTAACGCCGGAATCCA 2549
                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mora M;
Scarselli M;
                                                                                  tgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcctggctgcatacgct 218
                                                                                                                                 gattatggtgggcggtggcctgtatctctgctggatgggttaccagatgctacgtggtgc 278
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253015 to 254536, 254577 to 254615, and Y74253 to Y75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 254537 to 254576 and 254616 to 255473 represent PCR
                                                                                                                                                                                279 actgaaaaaagaggcggtttctgcacctgcgccacaggtcgagctggcgaaaagtgggcg
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                                                                                                                                                                                                                                                                                                                                                                                       Neisseria gonorrheae ORF 589 partial DNA sequence SEQ ID NO:1827
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                                    Length 3288;
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Scalato E, S
                                                           Indels
                                                                                                                                                                                                                                           2548 TIGITICTITAGIGGCAGCIIGACTATICACGCIGICACAAACG 2505
Sequence 3288 BP; 894 A; 793 C; 768 G; 833 T; 0 other;
                                                                                                                                                                                                                              339 cagtttcctgaaaggtttactgaccaatctcgctaatccgaaag 382
                                  Score 32; DB 18; L
Pred. No. 3;
0; Mismatches 120;
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Ratti (
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, Pizza M, Rappuoli R,
                                  5.28;
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98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
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                                                                                                                                                                                                                                                                                                                Z53939 standard; DNA; 2178
                                                                                                                                                                                                                                                                                                                                                                21-MAR-2000 (first entry)
                                                          Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pizza M, 1
Venter JC;
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P-PSDB; Y75177.
                                              Similarity
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
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09-OCT-1998;
09-OCT-1998;
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Tettelin H,
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                                    Query Match
                                                 Local
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                                                                                                                                                                                                                                                                                          RESULT 10
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primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polyuucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.6; DE Pred. No. 3.4; 0; Mismatches
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les 55; Conserv
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<pre>base numbering given in the specification" = v "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"</pre>	<pre>"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" "</pre>	"this nucleotide is represer specification, and is inclubase numbering given in the	"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" " this nucleotide is represented as a * in the specification, and is included to maintain the specification, and is included to maintain the	=	ab this nucleotide specification, base numbering ac this nucleotide	specification, and is inclubase numbering given in the ad "this nucleotide is representables numbering given in the base numbering given in the	<pre>"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" a af "this nucleotide is represented as a * in the specification, and is included to maintain the base and is included to maintain the control of the</pre>	base numbering given in the specification ag "this nucleotide is represented as a * in specification, and is included to mainta base numbering given in the specification ah	<pre>- "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" - ai - "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" - aj</pre>
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"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
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                                                                                                                                                                         5;
                                                                                                                                               Length 5059;
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                                                                                                                                                Match 5.1%; Score 31.6; DB 20;
Local Similarity 13.4%; Pred. No. 5.1;
ess 57; Conservative 176; Mismatches 189;
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                                        misc_difference 3860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ttttggtcaaacacatgtgattgcaagcggcccagaggatgccccgccgcttgtattact 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                            The DNA fragment encoding carboxyl esterase (CE) in B.subtilis Thai 1-8 (CBS 679.85) (Bell-HindIII fragment of 2kb originating from pNAPT-2 (see EP-233656)) was cloned into vector pTZ18R. Single-stranded DNA was prepared and subjected to oligonucleotide directed mutagenesis. Eleven different mutagenesis reactions were performed in order to substitute the 11 yaine residues of CE one at the time by a glutamine residue. The resulting mutant esterase was produced in E.coli DHI (ATCC 33849) and tested for stability in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence of (S)-naproxen. The wild type enzyme is encoded by a DNA at least 70% homologous with this sequence (NNN-Lys in the wild type.) and is itself 70% homologous to the B subtilis esterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                     Stabilised carboxyl esterase used for hydrolysis of S-naproxen obtd. by substituting or modifying basic residues of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 903 BP; 227 A; 194 C; 191 G; 258 T; 33 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.2;
Pred. No. 3;
                                                                                                                                                Disclosure; Fig 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                 WPI; 1990-329202/44
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Matches 105; Conserv
                                     P-PSDB; R07532
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Best Local S
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                                                                                                              enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
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The present sequence is that of open reading frame (ORF) mtbn6 (partial) of Mycobacterium tuberculosis. This is 1 of 8 ORFs (see A89075-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. The proteins encoded by these ORFs, i.e. MTBNN-8 (see B19842-49) represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, of or diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA concoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic concoding methods.
                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                                (PUBL-) PUBLIC HEALTH RES INST NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 2; 35pp; English
                                                                                              04-MAY-2000; 2000WO-US12257.
                                                                                                                                                99US-0132505
                                                                                                                                                                                                                                                                                            WPI; 2001-007153/01.
P-PSDB; B19847.
WO200066157-A1.
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                                                                                                                                                04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-1998
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                                                  09-NOV-2000
                                                                                                                                                                                                                                                  Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T33535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCG
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directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, coding and
initiation codons, genomic flanking regions, intron-exon borders, the
initiation codons, genomic flanking regions, intron-exon borders, the
5'-end, the 3'-end and the juxta-section between coding and non-coding
regions and all segments of RNAs encoding proteins associated with one
or more diseases, conditions or mixtures. The antisense oligonucleotides
configuration or mixtures. The antisense oligonucleotides
in may be derived from sequences X55272-74. These multiple target
oligonucleotides (specifically X5180-271) can be used for the antisense
treatment of diseases and conditions. Typical diseases and conditions
are those associated with impaired respiration and inflammation,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
respiratory distress syndrome, pain, cystic fibrosis, pulmonary
reprirension, pulmonary vascoconstriction, employsema, chronic obstructive
pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
carcinomas e.g. colon cancer, breast cancer, lung cancer, parcreatic
metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                       New antisense oligonucleotides used in treatment of, e.g. \operatorname{pulmonary} vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis open reading frame mtbn6, partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTBN6; tuberculosis; BCG; vaccine; infection; diagnosis; ds.
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37;
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Pred. No. 37;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 37; 120pp; English.
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                          98WO-US19419.
                                                                    98US-0093972.
                                                                                                                                                UYEC-) UNIV EAST CAROLINA
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/partial
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Best Local Similarity
Matches 47; Conserv
                       17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-2001
                                                                         09-JUN-1998;
                                                                                                 17-SEP-1997;
                                                                                                                                                                                                   Nyce JW;
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440 ccgcgcgctggggcatttttgcgctgatcattgtcgaaacgctggcgtggtttaccgtcg 499
                                                                                                                                                          Gaps
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obacteria; vaccine; infection; marker; ss.
                                                                                               0;
                                                         Length 1536;
                                                                                                 Indels
Sequence 1536 BP; 224 A; 473 C; 519 G; 320 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
2327..11126
/*tote= "BCG delta 1 deletion region"
                                                         5.0%; Score 30.8; DB 22; 58.9%; Pred. No. 5.2;
                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCG deletion region 1 and flanking sequences.
                                                                                               0; Mismatches
                                                                                                                                                                                                                     500 ttgccagcctgtttgccctgccgcaaatgc 529
                                                                                                                                                                                                                                             T33535 standard; DNA; 16885 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis strain BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                         Query Match
Best Local Similarity 58.9
Matches 53; Conservative
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This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdeltal. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see T35353 and T3537) have also been detected. Identification involved screening a BCG cosmid library with a radionabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an virulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see T3358-46), or by checking the presence or absence of absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                              Detecting markers for avirulence in Mycobacterium – used in
production of vaccines against bacterial infection, and to detect
bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16885 BP; 3050 A; 5603 C; 5307 G; 2915 T; 10 other;
                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 66pp; English.
                                         96WO-US01938
                                                                               95US-0390878
                                                                                                                         (PATH-) PATHOGENESIS CORP.
                                                                                                                                                                   Stover CK;
                                                                                                                                                                                                      WPI; 1996-393419/39.
                                                                                                                                                                 Mahairas GG,
                                         15-FEB-1996;
                                                                               17-FEB-1995;
  22-AUG-1996
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0; 0; Gaps 37; Indels Query Match 5.0%; Score 30.8; DB Best Local Similarity 58.9%; Pred. No. 17; Matches 53; Conservative 0; Mismatches 500 ttgccagcctgtttgccctgccgcaaatgc 529 q õ

DB 17; Length 16885;

7990 cggtcgcgcggatcgcgctgccgcattc 8019

Search completed: May 6, 2001, 16:27:58 Job time: 2659 sec

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RESULT 2
US-08-390-878-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 539,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 13, Sequence 53, Sequence 18, Sequence 18, Sequence 18, Sequence 118, Sequence 118, Sequence 126, Sequence 126,
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Sequence 1
Sequence 1
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Sequence 9
Sequence 1
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Sequence 7
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-13-118-126

US-08-409-53

US-08-413-416-126

US-08-413-416-126

US-08-413-418-126

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                                                                                                                                                                             US-09-466-935-3_COPY_187_804
                                                                     nucleic search, using sw model
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Sequence 539, Application US/09060756

Sequence 539, Application US/09060756

Sequence 539, Application US/09060756

Sequence 539, Application US/09060756

Sequence 539, Application

APPLICANT: Cole, Stewart

APPLICANT: Cole, Stewart

APPLICANT: Goldon, Stephen

APPLICANT: Billault, Alain

TITLE OF INVENTION: HERHOR OF A MYCOBACTERIUM USING A BAC-BASED DNA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

CURRENT APPLICANTON NUMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 539
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Patent No. 5706683
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 431;
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0.34;
US-08-996-685-7
US-08-981-478-1
US-08-980-179-2
US-08-880-179-2
US-08-800-179-1
US-08-80-179-1
US-08-952-874-1
US-09-95-97-2
US-09-96-623A-16
US-09-126-623A-17
US-09-126-635A-20
US-08-96-635A-20
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Pred. No. 0.34
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Best Local Similarity 50.0
Matches 78; Conservative
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CLASSIFICATION:
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Patent No. 617086
CENERAL INFORMATION:
APPLICANT: Riley, Lee W.
APPLICANT: Nathan, Carl F.
APPLICANT: BLT, Sabine
TITLE OF INVENTION: DNA MOLECULE CONFERRING ON MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS RESISTANCE AGAINST ANTIMICROBIAL REACTIVE
TITLE OF INVENTION: OXIGEN AND NITROGEN INTERMEDIATES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: CLIATOR SQUARE, P.O. BOX 1051
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Town Market Plaza, Steuart Street Tower, 20th
STREET: Ploor
CITY: San Francisco
STATE: California
COUNTRY: GSA
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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APPLICATION NUMBER: US/09/067,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) US-08-390-878-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.0%;
Best Local Similarity 58.9%;
Matches 53; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: New York
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GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
APPLICANT: RAILey, Lee W.
APPLICANT: Nathan, Carl F.
APPLICANT: Nathan, Carl F.
APPLICANT: Intt, Sabin Carl F.
APPLICANT: CARL F.
APPLICANT: SABIN CARL F.
APPLICANT: CARL F.
APPLICANT: CARL F.
TITLE OF INVENTION: TOYGEN AND NITROGEN INTERMEDIATES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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4.9%; Score 30.2; DB 4; Length 1244;
Best Local Similarity 49.7%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 78; Indels 0.
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/09/067,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 ctgcgccacaggtcgagctggcgaaaagtgggcgc 339
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APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MAY-1997
ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 15603/491
FELECOMMUNICATION INFORMATION:
TELEFARE (716) 263-1304
TELEFAR: (716) 263-1304
TELEFAR: (716) 263-1304
TELEFAR: (716) 263-1304
TELEFAR: (716) 263-1304
TELEFAR: (716) 263-1304
TELEFAR: (716) 263-150
SEOURICE CHARACTERISTICS:
LENGTH: 1244 base pairs
TYPE: nucleic acid
STRANDENNES: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MAX-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09067626
; Patent No. 6177086
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-067-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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NAME/KEY:
LOCATION:
                                         NAME/KEY:
; LOCATION:
US-07-941-651-1
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US-08-279-996-1
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                                                                                                                                                                                                                                                                                                                                                                  245 tctgctggatgggttaccagatgctacgtggtgcactgaaaaaaagaggcggtttctgcac 304
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                                                                                                                                                                                                                                                                                   Query Match
4.9%; Score 30.2; DB 4; Length 1244;
Best Local Similarity 49.7%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 78; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Boston, Rebecca S.
APPLICANT: Bass, Henry W.
APPLICANT: Bass, Henry W.
APPLICANT: O'Erian, Gregory R.
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENT POUNT DO NOT SOFTWARE SOFTWARE PATENTIAN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,651
FILING DATE: 19920908
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
REFERENCE/DCOKET NUMBER: 5051-199
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 ctgcgccacaggtcgagctggcgaaaagtgggcgc 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            770 cceacigecceargergcreeccecersrcccac 804
REFERENCE/DOCKET NUMBER: 19603/491
TELECOMMONICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1304
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charlotte
: No. 5332808th Carolina
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/07941651
Patent No. 5332808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEKAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1934 base palrs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA US-09-067-626-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-07-941-651-1
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                                                                                                                                                                                                                                                            218 tgattatggtggggggtggcctgtatctctgctggatgggttaccagatgctacgtggtg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1696 ACAGGATCTCGAAAGCCGTCTTCAGGTGGGCCGTCGACCCGACCGCTGAGATC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                             338 gcagtttcctgaaaggtttactgaccaatctcgctaatccgaaagcgattatc 390
                                                                                                                                                            4.7%; Score 29; DB 1; Length 1934;
48.0%; Pred. No. 4.6;
tive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boston, Rebecca S.
APPLICANT: Bass, Henry W.
APPLICANT: O'Brian, Gregory R.
TITLE OF INVENTION: Drotein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ANDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/279,996
FILING BATE: 25-UUL-1994
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,651
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sibley/ Kenneth D.
REGISTRATION NUMBER: 31.665
REFERENCE/DOCKET NUMBER: 5051-199
TELECHONE: 919-881-3140
TELECHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITALE: Charlotte
STATE: No. 5552140th Carolina
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08279996
; Patent No. 5552140
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
MOLECULE TYPE: DNA (genomic)
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TELEX: 575102
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1934 base pairs
                                                                                                                                                               Query Match
Best Local Similarity 48.09
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
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                                                CDS
990..1826
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2166 GCTGGTGGACCCTACGGTCCAGGTGGTGCTGGACCCTACGGACCAGGTGGTGCTGGT 2225
               120 gggcgtgctgggcattacctgcggcgtaatggtttgggctgggattgcgctgctggct 179
                                                                                                                                                                                         240 gtatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaaagaggcggtttc 299
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                                                                                                      180 gcatttgattatcgaaaaaatggcctggctgcatacgctgattatggtggcggtggcct
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                                                                                                                                                                                                                                                                                                  300 tgcacctgcgccacaggtcgagctggcgaaaagtgggcgcagttcctg 348
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US-08-680-726A-53

Sequence 53, Application US/08680726A

Batent No. 5804197

GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
ITILE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES; NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-UL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 2618-46-C1
FELERHONE: (303) 863-9700
TELERHONE: (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-9700
TELERA. (303) 863-923
TELERA. (303) 863-923
TELERA. (303) 863-923
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1700 Lincoln Street, Suite 3500 CITY: Denver STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80203
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US-08-680-726A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                           1636 TCAAGAAGCCGCAAGCGGTGACCATATCGGCGCTGGAGGGGGAAGCAGGTGCAGAAATGGG 1695
                                                                                                                                                                                                                                  278 cactgaaaaaaaaagagggtttctgcacctgcgccacaggtcgagctggcgaaaagtgggc 337
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lewis, Randolph V
APPLICANT: HAYASH, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                               1696 ACAGGATCTCGAAAGCCGTCTTCAGGTGGGCCGTCGACCCCGACCGCTGAGATC 1748
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0
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                                                           4.7%; Score 29; DB 1; Length 1934;
48.0%; Pred. No. 4.6;
Live 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 2830;
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Pred. No. 5.7;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REFERENCE/DOCKET NUMBER: 28977
REFERENCE/DOCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOLASCH & BIRCH SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KC
STREET: 8110 GATEHOUSE RD. SU
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
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                                                           Query Match
Best Local Similarity 48.0°
Matches 83; Conservative
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Best Local Similarity 45.4
Matches 104; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : NAME/KEY:
; LOCATION:
US-09-010-928B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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US-08-279-996-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 ggotgcatacgctgattatggtgggcggtggcctgtatctctgctggatgggttaccaga 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 TGATGAATTGGGATTAGTTTTAGCTGCCCCCGCTCCATTTAATCAAGGTCAATATAGACG 476
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477 GGTTATTCAAATTGAAAATGAAGTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 536
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                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application US/09092409
Patent No. 6159478
GENERAL INFORMATION:
APPLICANT: Hand, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMETEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.4; DB
Pred. No. 5.2;
0; Mismatches
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CLASSIFCATION
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPOINTED TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE 
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                                                                                                                                                           537 AACTIGITATITITICTAAAGAA 558
                                                                                 266 tgctacgtggtgcactgaaaaa 287
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Best Local Similarity 50.0%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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; LOCATION: 1..1
US-09-092-409-53
                                                                                                                                                                                                                                                                                   RESULT 9
US-09-092-409-53
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US-08-413-118-18
Sequence 18, Application US/08413118
SEQUENCE INFORMATION:
NUMBER OF INVENTION:
NUMBER OF SEQUENCES: 128
SEQUENCES: 128
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                     APPLICANT: Paclett, Enzo
APPLICANT: Limbach, Keith J.
ATILE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 ggctgcatacgctgattatggtgggcggtggcctgtatctctgctggatgggttaccaga 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617 TGATGAATTGGGATTAGTTTTAGCTGCCCCCGCTCCATTTAATCAAGGTCAATATAGACG 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
APPLICATION NUMBER: US/08/220,151
APPLICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REGISTRATION NUMBER: 454310-2540
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
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TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
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Pred. No. 5.9;
0; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-220-151-18; Sequence 18, Application US/08220151; Patent No. 5529780; Patent INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        737 AACTIGITATITITICIAAAGAA 758
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.09
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                  USA
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; MOLECULE TYPE:
US-08-220-151-18
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
RESISTAATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
                                                                                                                                                                                               454310-2670
                  CLASSIFICATION:
CCASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,118
FFILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,556
REFERENCE/DOORET NUMBER: 454310-
TELECOMMUNICATION INFORMATION:
TELEFHOME: (212) 840-0712
TELEFANE: (212) 840-0712
TELEFANE: (212) 840-0712
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TRUCTH: 1320 base pairs
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29-MAR-1995
APPLICATION NUMBER: US/08/473,446
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: CDNA US-08-473-446-18
                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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PAPLICANT: LIMBACH, KETTH J.

TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR CORRESPONDENCES: 128

ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FITH AVENUE, 25TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 taatggtttggggttggggttgggcttggcttgatttgattatcgaaaaatggcct 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 GGTTATTCAAATTGAAAATGAAGTTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 28.4; DB 1; Length 1320; 50.0%; Pred. No. 5.9; ive 0; Mismatches 71; Indels 0
                                                            ZIP: 10036

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE:: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   FILING PADE: 27 FRANT 1532
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: FROMMER: WILLIAM S.
REGISTRATION NUMBER: 25,506
RECISTRATION NUMBER: 25,506
RETERPORE/POCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
TELEFONDE: (212) 840-3333
TELEFONDE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LEMOTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDBRESS: single
                NEW YORK: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK COUNTRY: UNITED STATES OF AMERICA ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-473-446-18
Sequence 18, Application US/08473446
Patent No. 6017542
GENERAL INFORMATION:
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Best Local Similarity 50.09
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear // MOLECULE TYPE: CDNA US-08-413-118-18
    NEW YORK
                                              COUNTRY:
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146 taatggtttggggctggattgcgctgcttggcctgcatttgattatcgaaaaatggcct 205
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                                                                                                                                                                                                       677 GGTTATTCAAATTGAAAATGAAGTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 736
                                                                                                                       617 TGATGAATTGGGATTAGTTTTAGCTGCCCCCGCTCCATTTAATCAAGGTCAATATAGACG 676
4.6%; Score 28.4; DB 3; Length 1320;
50.0%; Pred. No. 5.9;
Live 0; Mismatches 71; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUPTRY: UNITED STATES OF AMERICA
ZIP: 10036
ZUR: 10036
COMPUTER REDABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
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Gaps

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5604 GGTTATTCAAATTGAAATGAAGTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 5663
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                                                                                                                                                                                                                                                                                             206 ggctgcatacgctgattatggtgggcggtggcctgtatctctgctggatgggttaccaga 265
                                                                                                                                                                      146 taatggtttgggctgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcct 205
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                                                                      Score 28.4; DB 3; Length 1415;
Pred. No. 6.2;
0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/08680726A
Patent No. 5804197
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hannes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Street, Suite 3500
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-UUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 26.18-46-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            836 AACTIGITATITITCTAAAGAA 857
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 51:
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LENGTH: 10592 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                     Query Match
Best Local Similarity 50.vv
These 71; Conservative
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Best Local Similarity 50.0%
Matches 71; Conservative
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MEDIUM TYPE: Floppy
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US-08-680-726A-51
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     US-08-473-446-126
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US-08-680-726A-51
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APPLICANT: LINBACH, KETTH J.
TITLE OF INVENTION: UNCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS GB, GC, AND GD AND USES THEREFOR NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 taatggtttgggctgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcct 205
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                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UNITED STATES OF AMERICA
ZIE: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S: CURTIS, MORRIS & SAFFORD, P.C. 530 FIFTH AVENUE, 25TH FLOOR
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NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
STRANDENESS: aligle
TOPOLICY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/473,446
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Patent No. 6017542
GENERAL INFORMATION:
LELETAX: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
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US-08-413-118-126
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  6, 2001, 14:41:24; Search time 1151.46 Seconds (without alignments) 4688.750 Million cell updates/sec
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		CNS0073W	AQ280480	BE793235	CNS00JX7	CNS006RB	CNSOOCNG	CNS0300A	CNS04744	CNS028DO	CNS01671	BF621090	CNS0062R	CNS017GJ	BE957648	AV720117	AW721077	BE196650	AQ438206
<u> </u>	9	229	204	139	229	229	229	231	231	230	229	150	229	229	142	32	119	164	206
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Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M3-21
Class: BAC ends.
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
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CalTech Human BAC Library D"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golde
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
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Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0200
                                                                           ch 6.2%; Score 38.6; DB 1 Similarity 20.7%; Pred. No. 0.37; 47; Conservative 83; Mismatches
                    221 t
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    /note="end : TET3"
95 c 109 q
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                                                                           Query Match
Best Local Si
Matches 47;
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AL Submitssion

BD irect Submission

Submitsted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : Seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkelsy Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitliy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and haron Amamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNR provided by the BDGP from the isogenic strain v2: cn bw sp., the same strain used for the BDGP's pl and bST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be Location/Quallifiers

Location/Quallifiers

Location/Quallifiers

NNESS | Location from the BACPAC Resource Center can be Location (1922)
AW678708 WS1.1_D12
AW678638 WS1.1_D12
AQ550746 RP2111-11
AL066286 Drosophil
A1384522 fb06a05.y
A1730513 BNLGH1693
BE284012 601103181
AL077673 Drosophil
AW729450 GA._Eb001
BE284012 601103181
AL065923 Drosophil
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AL06592 Drosophil
AL065923 Drosophil
AL065923 Prosophil
AL06592 Drosophil
AL06592 Drosophil
AL06592 GTEATOGON
AL310754 TEATOGON
AL1310764 GTEATOGON
AL131074 TEATOGON
AL131074 GTEATOGON
AL168689 Ox70007.s
A176849 CSTA15098
BE107761 601823751
AL068242 Drosophil
BB45980 ESTA15098
BE107761 601823751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS0073W 922 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
Lly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                   BB089204
AQ36581
CNS006U0
CNS04DR2
BG030901
BE729153
CNS051EH
CNS05D6R
AI168689
                                                                                                                                                                                                                                                                                                                    BE459806
BF107761
CNS00LI0
                                                                                          AI730513
BE284012
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AW729450
BF273544
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Drosophila melanogaster
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COMMENT

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- Web: www.genoscope.ons.fr

- Web: www.genoscope.ons.fr

- Determination of this BAC-end sequence was carried out as part of a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                              CNSOOJX7 977 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC;
BACK39C01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
cttggcctgcatttgattatcgaaaaatggcctggctgcatacgctgattatggtgggc 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 agaagcgatgatgggcgtgctgggcattacctgcggcgtaatggtttgggctgggattgc 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Ptersygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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17.1%; Pred. No. 2.9;
Live 66; Mismatches
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/note="end : TET3"
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Drosophila melanogaster
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Matches 22; Conservative
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1 (bases 1 to 1108)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/Link at: image.llnl.gov

Plate: LLCM/84 row: d column: 20

High quality sequence stop: 719.
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                                                                                                                                                                                                                                                     tgggcgtgctgggcattacctgcggcgtaatggtttgggctgggattgcgctggcttggcc 178
                                                                                                               241 TGGGCTAGCCCAGGATCGGCTGGTGGGAGGTAGCTGCACTGGGGGGATGTGAGGGGTT 182
                                                                                                                                                            179 tgcatttgattatcgaaaaaatggcctggctgcatacgctgattatggtgggcggtggcc 238
                                                                                                                                                                                                        181 GGCATTGCAGGACCTTCCATGCCGCCTGCCTCCATCTGGGGCCAGGAGTTGGCCCTGGGC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE793235 1108 bp mRNA EST 20-SEP-2000 601583674F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937891 5'
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                           Gaps
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  Pred. No. 0.35;
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49.08;
Best Local Similarity 49.03
Matches 102; Conservative
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Best Local Simi
Matches 74;
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AUTHORS
TITLE
JOURNAL
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Direct Submission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr
- Gollaboration with the Berkeley Drosophila Genome Project (BDGP).

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NY. The library is named RPCI-98 and was constructed by partial
sogenic strain of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
and how to order indyvidual BAC clones, the entire library or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Tetraodon nigroviridis.

Tetraodon nigroviridis

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Eurypteryqii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
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end of clone
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                     fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 939)
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Tetraodon nigroviridis genome survey sequence T7
041G19 of library G from Tetraodon nigroviridis,
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/db_xref="texon:\227"
/clone_lib="RPCI-98"
/clone="BACR26H16"
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AL252739.1 GI:7973751
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Best Local Similarity 8.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Print Juvo Evyn Cedea. France (E-Mall: sequergenoscope.cns.IT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL059400
AL059400.1 GI:4946964
                                                                                               CNSO06RB 912 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14L21 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    789 SKSGTBYTBYKKCKTKKTYKTGTTTTTCKTTTTTTKKBKBTGTTGTBGKTGTYSTKBKT 730
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 912)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI4L21"
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                          Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Cherier, and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using
                                                                  Bouneau, L., Fisher, C.,
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei
Eurypterygii, Ctenosquamata, Acanthomorpha, Euacanthomorpha,
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fishe Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="086H24"
/clone_lib="G"
/orde="Genoscope sequence ID : COBK
/ 295 c 269 g 212 t 2
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0; Mismatches
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Best Local Similarity 54.7%;
Matches 70; Conservative C
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                             2 (bases 1 to 914)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lar
scale clone-and sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="G"
/note="Genoscope sequence ID : COBG041AD10LP1-end : T7"
| 242 c 293 g 175 t 3 others
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086H24 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="041G19"
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Pred. No. 4.3;
O; Mismatches
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Tetraodon nigroviridis.
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BF621090 835 bp mRNA EST 18-DEC-2000
HVSWE20003P06f Hordeum vulgare seedling shoot EST library
HVDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0003P06f,
mRNA sequence.
BF621090
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Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y. Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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/db_xref="taxon:4513"
/db_xref="taxon:4513"
/clone="HYSMEA0003P06f"
/clone=lib="Hordeum vulgare seedling shoot EST
HYCDNA0001 (Cold stress)"
/lasue_type="Seedling shoot"
/lab_host="TJC121"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Hordeum vulgare"
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High quality sequence start: 8
High quality sequence stop: 515.
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/clone="BACN15022"
/note="end : SP6"
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                                                                                                         Direct Submission
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraddon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraddon.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
Br 191 91006 EVRY cedex - FRANCE (E-mail: segrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/note="Genoscope sequence ID : COAG244CF06SP1-end
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/organism="Drosophila melanogaster"
/plasmid="plealoabCil"
/db_xref="taxon:7227"
/clone_lib="brosbAC"
                                                                                                                                                                                                                                                                                                                                                /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="244L11"
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Pred. No. 4.5;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley brosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
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                                                                                                                  198 TGGATTACCGGCGTTGACAGATCCCCCCCCCCCCCCACGCACAACCTTGATGAGCAACCT 257
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                                                         Gaps
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 920)
                                                                                             487 tggtttaccgtcgttgccagcctgtttgccctgccgcaaatgcgccgtggttatcaacgt
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/db_xref="taxon:7227"
                DB 150;
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/note="end : TET3"
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              5.6%;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Drosophila melanogaster genome survey sequence SP6 end of BAC BACNIYNI8 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Pred. No. 8.1;
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/clone="BACN17N18"
/note="end : SP6"
a 178 c 76 g
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completed: May
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/db xref="taxon:9606"
/clone="lmAGE:8836706"
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/tissue_type="from acute myelogenous leukemia"
/tab_nost="bH10B (TI phage-resistant)"
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/rote="organ: bone marrow; Vector: pDNR-LIB (Clontech);
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sequence: 5'-ATTCTAGAGCCCGAGGGGGCACACATG-(130)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies
contrained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (palo Alto, CA)."
1 others
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                                                                                                                                                                                                                                                                                                                                                                        L (bases 1 to 0832)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Oct 3, 2000 this sequence version replaced gi:10568353.

Contact: Robert Strausberg, Ph.D.

Tel: (301, 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM525 row: p column: 05

High quality sequence stop: 2.

Location/Qualifiers
                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 832)
                                                                                                                                    BE957648 832 bp mRNA EST 14-DEC-2000 601653724R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838708 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS AV720117 501 bp mRNA EST 16-OCT-2000 DEFINITION AV720117 GLC Homo sapiens cDNA clone GLCFEF09 5', mRNA sequence.
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tive 0; Mismatches 38; Indels 0;
Db 1058 ISYGYTGYGGGGCGTGKCTSTTGTGTGTGGKSSBKKGGCTG 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 tcgagctggcgaaaagtgggcgcagtttcctgaaa 351
                                                                                                                                                                                                                          BE957648.2 GI:11774115
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Best Local Similarity 60.09
Matches 57; Conservative
                                                                                                                                                                                mRNA sequence.
BE957648
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Homo sapiens
Butazoca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)
Glan, B., Wul, T., Hang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,
Xu, X., Lii, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,
Xu, S., Gu, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang
Homo sapiens cDNA GLC clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GLCEEF09"
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/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Addilt"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
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/db_xref="taxon:9606"
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AV720117
AV720117.1 GI:10817269
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

6, 2001, 14:38:48 ; Search time 34.23 Seconds
 (without alignments)
 344.015 Million cell updates/sec Мау

Run on:

US-09-466-935-4

1054 1 MLMLFLTYAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

390729 seqs, 57163235 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

390729

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A. Selicseq. (401: **)

2. (SIDSZ/gcgdata/geneseqp/AA1980.DAT: **)

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	E. coli L-threonin	Escherichia coli Y	Escherichia coli Y	A. vitis hypersens	E. coli L-ĥomoseri	E. coli RhtB prote	C. qlutamicum Lys	Escherichia coli Y	Escherichia coli Y	Human ORFX ORF171	Mel-linked mlgA ge
	;	10	X99598	B01786	B01787	B11637	X99597	Y79298	W37715	B01789	B01788	B40407	R87527
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æ	Query	March	100.0	24.8	18.0	17.0	11.6	11.6	10.0	9.6	9.6	9.0	8.6
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W73358 R98004 W34528 R05475 Y38893	~ # ~ ~ # 6	W88447 R03463 W90237 W90236 Y38890	B08549 R99255 Y16099 Y34112 Y30312 Y29662	X30311 Y29661 Y10826 Y44344 Y29796 W90938 Y51928
20 17 11 20 20	22222	70 70 70 70 70 70 70 70 70 70 70 70 70 7	200000	222222
153 431 431 390 356 713	444 444 555 900 900 900	1170 381 299 306 356 356	1518 1518 332 332 332 332 859	859 874 898 898 914 941
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12 14 15 16	18 7 2 2 1 1 8 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	400000 40000		337 338 444 5443 5443

## ALIGNMENTS

RESULT

Tokhmakova IL; Aleshin VV, Belareva AV, L-threonine resistance; L-threonine synthesis; rhtC; L-homoserine; L-valine; L-leucine. E. coli L-threonine resistance protein, RhtC. Ä. Y99598 standard; Protein; 206 99EP-0125406. Livshits VA, Zakataeva NP, 98RU-0123511, (first entry) (AJIN ) AJINOMOTO KK. Escherichia coli. 20-DEC-1999; 23-DEC-1998; EP1013765-A1 08-SEP-2000 28-JUN-2000 Y99598; Y99598 

Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -

WPI; 2000-414602/36. N-PSDB; A48443.

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Claim 1; Page 19; 29pp; English.
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                                                                                                                                                    Conservative
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                                                                                                                                         Best Local Similarity
Matches 58; Conserv
                                                                                                   223 AA;
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Tokhmakova IL;
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion protein .
                            L-threonine
                The present sequence is the L-threonine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                           amino acid production; excretion protein gene;
                                                                                                                                                                                                                 1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL
                                                                                                                                                                                                                                                                    TNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGY
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                                                                                                                                                                         Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli YahN amino acid excretion protein.
                                                                                                                                                                       100.0%; Score 1054; DB 21;
100.0%; Pred. No. 1.9e-112;
ive 0; Mismatches 0;
                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                   QRLAKWIDGFAGALFAGFGIHLIISR 206
1; Page 15-16; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                             B01786 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli; yahN gene; amino aci
amino acid excretion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98RU-0124016
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Best Local Similarity 100.
Matches 206; Conservative
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N-PSDB; A52688.
                                                                                                                                           206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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Tokhmakova IL;
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                                                                                                                                            Sequence
Claim
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The present sequence is the YahN amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of it gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 itqceeifslirivggayllwfawcsmr----rqstpqmstlqqpisapwyvffrr 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRS-----FLK 117
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the YeaS amino acid excretion protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid production; excretion protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                                             4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI
                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                            Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli Yeas amino acid excretion protein.
                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                         24.8%; Score 261.5; DB 21; 28.2%; Pred. No. 6.5e-22; tive 50; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakanishi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGYQRLAKWIDGFAGALFAGFGIHLI 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B01787 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli; yeas gene; amino acamino acid excretion protein
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Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, valine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences B11630-B11688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nuclocide sequences (A61501-A61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                                                                                                                                                                                                                                                                                   68 AWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK 127
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                        --- VMVWAGIALLGLHLIIEKM 67
                                                                                                                                                                                                                                                                                                                                           128 AIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAW-----FTVVASLFALPQMRRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant.
                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. vitis hypersensitive response elicitor protein, SEQ ID NO:9.
                                                                                                                                                         Length 212;
                                                                                                                                                                                      Indels
                                                                                                                                                         Score 190; DB 21;
Pred. No. 8.8e-14;
                                                                                                                                                                                                                      IVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG--
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 85-86; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B11637 standard; Protein; 229 AA.
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                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                      181 QRLAKWIDGFAGALFAGFGIHL 202
                                                                                                                                                                                                                                                                                                                                                                                                                        ::||| : | :| || kklakvgnsliglmfvgfaarl 207
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                                                                                                                                                         18.0%;
28.2%;
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                                                                                                                                                                                      57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376567/32.
                                                                                                                                                                         Local Similarity
                                                                                                           212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200028056-A2
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                                                                                                              Sequence
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                                                                                                                                                          Query Match
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occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLANPKAIIYFGSVFSLFVGDNVGTTAR--WGIFALIIVETLAWFTVVASLFALPQMRRG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 KMAWLHTLIMVGGGLYLCWMGYQMLRGALKK----EAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-homoserine resistance; L-homoserine synthesis; rhtB; L-threonine; L-valine; L-leucine.
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95;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.5e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       17.0%; Score 179.5; 27.0%; Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 YORLAKWIDGFAGALFAGFG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y99597 standard; Protein; 205
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 27.0%
54; Conservative
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N-PSDB; A48442.
                                                                                                                                                                                                                                                                                                                                                     229 AA;
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Best Local S
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                                                                         The present sequence is the L-homoserine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-homoserine resistance on E. coli bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated and no acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
         Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine,
                                                                                                                                                                                                                                                                                                                                                                                           117 KGLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQM 176
                                                                                                                                                                                                                                                                                                                                              61 HLII--EKMAWLHTLIMVGGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                    66 rsviafevlkw-----agaayliwlgiqqwraagaidlkslastgsrrhl-----fg 112
                                                                                                                                                                                                                                                                                                                                                                                                          ----MVWAGIALLGL 60
                                                                                                                                                                                                                                                                                                                        11 ltsiiltlspgsgaintmttslnhgypag----gvycwasdrtgdsycagwrgvgtlfs 65
                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homoserine resistance; RhtB protein; L-homoserine; L-alanine;
L-isoleucine; L-valine; L-threonine.
                                                                                                                                                                                                                                                    Length 205;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belareova AV;
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                                                                                                                                                                                                                                                                           89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 122, DB 21;
Pred. No. 4.9e-06;
36; Mismatches 89;
                                                                                                                                                                                                                                                                                                   10 MVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                       177 RRGYQRLAKWIDG------FAGALFAGFGIHLIISR
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                      to enhanced RhtC protein activity, us 
L-homoserine, L-valine and L-leucine
                                                      2; Page 13-14; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y79298 standard; Protein; 205 AA
                                                                                                                                                                                                                                                  11.6%;
21.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98RU-0118425
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                                                                                                                                                                                                                                                               Local Similarity 21.0%
nes 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-273530/24.
                                                                                                                                                                                                                   205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli.
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Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2000
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                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                      Query Match
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                                                       Claim
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Novel RhtB protein, useful for generation of L-homoserine resistance in Escherichia bacteria and large-scale production of e.g. L-homoserine and L-alanine \dot{}
                                                                                                                                                                                                                              The protein, RhtB, which participates in resistance to L-homoserine.

The protein, RhtB, which participates in resistance to L-homoserine.

Amplification of the rhtB gene (see 294405) results in an improvement of the amino acid productivity of E. coll. The invention provides: a protein comprising the present sequence or including a deletion, substitution, insertion and/or addition of 1 or more amino acids and having the activity of making a bacterium resistant to L-homoserine; DNA encoding RhtB; a bacterium, especially of the genus Escherichia, in which L-homoserine cresistance is enhanced by amplifying the copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an amino acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of L-homoserine, L-alanine, L-isoleucine, L-valine or L-threonine (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            export protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 rsviafevlkw-----agaayliwlgiqqwraagaidlkslastqsrrhl-----fg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HLII--EKMAWLHTLIMVGGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --tivodiivmigy 164
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11 ltsilltlspgsgaintmttslnhgypag----gvycwasdrtgdsycagwrgvgtlfs
                                                                                                                                                                                                           present sequence is that of the novel Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. glutamicum Lys E protein (lysine export protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 122; DB 21;
21.0%; Pred. No. 4.9e-06;
Live 36; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 MVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 RRGYQRLAKWIDG------FAGALFAGFGIHLIISR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:| || | :| || | 105 atlaqrialwikgpkqmkalnkifgslfmlvgallasar 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                            Claim 1; Page 11-12; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95DE-1048222
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nes 46; Conservative
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Matches
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B01788 standard; Protein; 195
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99RU-0104431.
            99RU-0104431,
98RU-0124016.
                                                        Zakataeva NP,
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                                 (AJIN ) AJINOMOTO CO INC
                                                                                                                          production of increasing the
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                                                                                        WPI; 2000-414802/36.
N-PSDB; A52691.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           211 AA;
                                                       Livshits VA, ;
Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1016710-A2
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09-MAR-1999;
30-DEC-1998;
            09-MAR-1999;
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                                                                                                                           Increased
                                                                                                                                       comprises
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                            This sequence is the LysE protein product, a lysine export protein. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, confinents and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                          60 vdllsnaapivldimrw-----ggiayllwfavmaakdamtnk---veapqiieetep 109
                                                                                                                                                                                                                                                                                                                                                                                                      LHL------IIEKMAWLHTLIMVGGLYLCWMGYQMLRGALKKEAVSAPAPQV----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tvpddtplggsavatdtrnrvrvevsvdkgrvwvkpmlmaivltwlnpnayldafvf1gg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 VFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIA-LLG 59
                                                                 Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli, yggA gene; amino acid production; excretion protein gene; amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ELAKSGRS--------FLKGLLTNLANPK----AIIYFGS
                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                            Length 236;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli YggA amino acid excretion protein.
                                                                                                                                                                                                                                                                                                            Score 105; DB 18;
Pred. No. 0.00051;
5; Mismatches 99;
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                                                                                                                          Claim 42; Page 10; 16pp; German.
                                                                                                                                                                                                                                                                                                                                    36;
           Vrlijc M;
                                                                                                                                                                                                                                                                                                            10.0%;
20.4%;
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                                                                                                                                                                                                                                                                                                                                    51; Conservative
           Sahm H,
                                 WPI; 1997-333867/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 FAGFGIHLII 204
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                           236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                             N-PSDB; T96816
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            Eggeling L,
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                                                                                                                                                                                                                                                                             Sequence
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The present sequence is the YggA amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                   of L-amino acids by an Escherichia bacterium
the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 A----NPKAIIYFGSVFSLFVGDNVGTTARWGIFAL-IIVETLAWFTVVASLFA--LPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRCALKKEAVSAPAPQVELAKSGRSFLKGLLTNL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli; yfik gene; amino acid production; excretion protein gene;
amino acid excretion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Nakanishi K, Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli YfiK amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%; Score 103; DB 21; ilarity 27.8%; Pred. No. 0.00075; Conservative 25; Mismatches 93;
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99US-0127607

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnetary; antipsoitatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialmamatory; antivaral; antibacterial; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antibacterial; onserving cancer; proliferative disorder; hypertension; neurodegenerative disorder; oscarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus crythematosus; infection; severe combined immunodeficiency; malarid; autofinmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage; damage; antiinflammatory disease; coagulation;
                                                                                                of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
                                                                                                                                                                                   The present sequence is the YfiK amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increased in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 LLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ---fslavidpaavh-llswagaayivwlawkiatsptkedglqa------kpisfw 108
                                                                                                                                                                                                                                                                                                                                                                              72; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG----VMVWAGIA 56
              Zakataeva NP, Nakanishi K, Aleshin VV, Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%; Score 101; DB 21; Length 195; 22.0%; Pred. No. 0.0012; tive 32; Mismatches 72; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF171 polypeptide sequence SEQ ID NO:342.
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                                                                                                                                                          Claim 1; Page 23; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 22.0%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive
                                                                                                                comprises increasing
protein -
                                                                                                  production
                                                     WPI; 2000-414802/36
                                                                                                                                                                                                                                                                                                        195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058473-A2
                                                                      N-PSDB; A52690
                            Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000
                                                                                                   Increased
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B40407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
B40407
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represent the human ORRY open reading frames 1 to 3161. The ORRY sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cadgulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antivingal; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; corpussive; antibacterial; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antithremmatic; antismedison or preventing or treating pathological conditions associated with an order cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astuma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; cenhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 YLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C74446 to C77606 encode the proteins given in B40237 to B43397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marine melA; selectable marker; oyater larva settlement; pigmentation; melanin; p-hydroxyphenylpyruvate-hydroxylase; mlgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%; Score 94.5; DB 21;
ilarity 25.7%; Pred. No. 0.0038;
Conservative 22; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 608; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R87527 standard; Protein; 153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mel-linked mlgA gene product.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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114 fatafaglglnlafag 129
                                                                                                                                                                                                  Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 AGALFAGFGIHLIISR
                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                 WPI; 2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 35; Conserv
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                                                                                                                                                                                                                                                                                                     N-PSDB; C74616.
                                                                                                                                                                                                     Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1996
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Best Local S
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Peptide
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                                                                                                                                                                                                                                                                                                                                                       99 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
                                                                                                                                                                                                                                                                                                                                                                43 LGITCGV--MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marine bacterium; melanin synthesis; marine exopolysaccharide;
                                                                                                                                                           Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing larval
                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                        The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colwelliana melA gene (T06765), and was designated migA (mel-linked gene). The role of the encoded protein (R87527) was unclear as deletion subcloning in E. coli demonstrated that only melA was required
                                                                                                                                                                                                                                                                                       8.6%; Score 91; DB 17; Length 153;
25.5%; Pred. No. 0.012;
ive 31; Mismatches 54; Indels
       Shewanella colwelliana strain LSTDYF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. colwelliana MlgA protein sequence.
                                                                                                                                                                                          Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                                                     (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                        148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                      pqlmvllsiimmt-effsmla 142
                                                                                                                                                                                                                                                                                                                                                                                                                                              W73358 standard; Protein; 153
                                                                    93US-0148945.
90US-0496804.
92US-0974837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MlgA; marine bacterıum; mela.
UV blocker; sunscreen; MelA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0476254
                                                     90US-0496804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewanella colwelliana
                                                                                                                    Weiner RM;
                                                                                                                                   WPI; 1996-039515/04.
N-PSDB; T06767.
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                 for melanogenesis.
                                                                                                                                                                                                                                                                  153 AA;
                                                                                                                                                                            oyster settlement
                                                                    08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                     21-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1999
                      US5474933-A
                                      12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS5846531-A
                                                                                                                    Fuqua WC,
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              W73358
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This sequence is the Shewanella colwelliana MigA protein, which is related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGITCGV--MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MelA melanin protein from marine bacteria – useful as UV blocker in e.g. cosmetics % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125..138
/label= 1003
/note= "immunogenic peptide 1003,
252..265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oestrogen-regulated gene; pLIV1; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oestrogen-regulated pLIV1 gene-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Fig 13; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMA-) UNIV MARYLAND BALTIMORE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R98004 standard; Protein; 431
95US-0476254.
90US-0496804.
92US-0974837.
93US-0148945.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuqua WC, Weiner RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-058995/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marker; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V08553
07-JUN-1995;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                   08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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Best Local
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 agvatl----aw---mvimgdglhnfsdglai--gaafteglssglstsvavfch 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 IVETLAWFTVVASLFALPQM-----RRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                    The polypeptide (R98004) encoded by a partial cDNA clone regions, 1003, 1004 and 1005, that were used to raise polyclonal antibodies in rabbits. Peptides 1004 and 1005, were most immunogenic, generating ELISA-positive sera at dilutions of 1/200000. Cross-reactivity studies using the 3 peptides intended 7 positive specific sera in tumnour samples from 74 patients with primary breast cancer. The pLIVI polypeptide was expressed in the cytosol of cestrogen receptor-positive epithelial cells of breast tumnours. Its presence can be used to predict the propensity for metastatic spread or the responsiveness of a breast tumnour to endocrine treatment. Its inactivation may be used as a means of treating breast cancer and metastasis.
                                                                                                                                                                                                                                                                                                                            Oestrogen-regulated pLIV1 gene and deduced polypeptide - useful for predicting the propensity for metastatic spread or the responsiveness to endocrine treatment of breast tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 431;
/label= 1105
/note= "immunogenic peptide 1005, claim 11
page 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AGIALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by pLIV1 gene partial sequence.
                                                                                                                                                                                                                               Green CD, Manning DL, Nicholson RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 86.5; DB
27.4%; Pred. No. 0.14;
tive 21; Mismatches
                                                                                                                                                                                                 (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 14-16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W34528 standard; Protein; 431
                                                                                                                                94CA-2132500
                                                                                                                                                                94CA-2132500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                              WPI; 1996-268987/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA;
                                                                                                                                                                                                                                                                             N-PSDB; T33219;
N-PSDB; T33220.
                                                                                                                                20-SEP-1994;
                                                                  CA2132500-A
                                                                                                  21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                 Gee JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W34528;
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This sequence is encoded by a partial sequence of the pLIV1 gene. This protein sequence is an oestrogen regulated gene associated with breast cancer. This sequence can be used in the method of the invention. The method is for determining the risk of metastasis of a female breast tunnour and predicting the responsiveness of a female breast tunnour comprising determining if a tissue sample from the tunnour expresses a polypeptide comprising at least 14 continuous amino acids of the protein encoded by this sequence. The method is useful for determining the risk of metastasis of a female breast tunnour and to predict the responsive of the female breast tunnour to hormone treatment. PLIV1 expression is highly predictive of tunnour coestrogen receptor expression and lymph node involvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 agvatl-----aw---mvimgdglhnfsdglai--gaafteglssglstsvavfch 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AGIALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSA------ 101
                                                                                                                                                                                                                                                                           Assessment of metastatic risk or oestrogen responsive-ness in breast cancer – by detecting expression of pLIV1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 IVETLAWFTVVASLFALPQM------RRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                Green CD, Manning DL, Nicholson RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 86.5; DB Best Local Similarity 27.4%; Pred. No. 0.14; Matches 49; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloramphenicol resistance; mutagenesis.
                                                                                                                                                                 (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloramphenicol resistance gene prod.
                                                                                                                                                                                                                                                                                                                         Claim 1; Column 5-10; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R05475 standard; protein; 390
                                                                                                                                     94US-0311023.
                                                                                                        94US-0311023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88DE-3841454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-1990 (first entry)
                                                                                                                                                                                                                            WPI; 1998-031740/03.
N-PSDB; T99070, T99071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 AA;
               Homo sapiens
                                                                                                        22-SEP-1994;
                                                                                                                                     22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1988;
                                           JS5693465-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                   See JMW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R05475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
R05475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366
qq
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Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 47; Conservative 35; Mismatches 78; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                94 LKKEAVSAPAPQVELAKSGRSFLKGLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 VL--GITCGVMVWAGI---ALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGA--- 93
                                                                                                                                                                                                                        When expressed in host cells this confers Chloramphenicol resistance on them.
                                                                                                                                                                                                                                                                                                                                                                1 MIMI,FLTVAMVHIVALMSPGPDFFFVSQ....-TAVSRSRKEAMMG 41
                                                                                                                                             Site specific mutagenesis of DNA at restriction enzyme positions by treating corresp. restriction fragments with hydroxylamine, and new mutated sequences and transformed microorganisms
                                                              Kassing F, Kalinowski J, Arnold W, Winterfeldt A, Puhler A;
Kautz P-S, Thierbach G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ALIIVETL----AWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1988; 88DE-3841454.
                                                                                                                                                                                                    Disclosure; ; p; German.
                                                                                                      WPI; 1990-186465/25.
NPSDB; Q04775.
                                      (DEGS ) DEGUSSA AG.
                                                                                                                                                                                                                                                                     390 AA;
                                                                                                                                                                                                                                                                       Sequence
q
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Db
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89 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 LGITCGV -- MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.6%; Score 91; DB 2; Length 153; Best Local Similarity 25.5%; Pred. No. 0.0064; Matches 36; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONDUTE: USA
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-UUN-1995
CLASSIFICATION: WUBBE: US/08/476,254
FILING CATENON: MASHER US/08/476,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C. STREET: 1400 K STREET NW
                US-08-716-873-2
US-08-477-451-12
US-08-805-118-3
US-08-724-394A-9
US-08-825-824-4
US-08-356-060A-34
US-08-46-090C-34
US-08-118-270-43
PCT-US93-08528-43
US-08-258-188-5
US-08-258-18-5
US-08-528-18-5
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US-09-231-227-2
US-07-816-283-2
US-07-816-283-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: POULOS III, JAMES A.
REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JAP30319C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
TELEFRA: 202 628-0088
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WELNER, RONALD M.
APPLICANT: FUGUA, WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08476254 Patent No. 5846531
, MOLECULE TYPE: protein US-08-476-254-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: WASHINGTON STATE: D.C.
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1 MLMLFLTVAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206
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US-09-097-759-3

US-09-183-25-4

US-09-183-25-4

US-09-183-25-4

US-09-183-25-4

US-09-183-25-4

US-09-22-837-2

US-08-22-74-10

US-09-26-214-11-6

US-09-26-214-14-14

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US-09-28-389A-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maxinum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match 1
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                          Seguence:
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                                                                                                                                                                                                                 Run on:
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11;

Gaps

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309 ELPHELGDFAVLLKAGMTVKQAVLYN-ALSAMLAYLGMATGIFIGHYAENVSMW-IFAL- 365
                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AGVATL------AW---AVINGDGLHNFSDGLAI--GAAFTBGLSSGLSTSVAVFCH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 GLH------LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVEL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 ----RPGALSALGAIAPPLAA---GAAFSALVLDRPLPS---GLFLGIVLSVTAVSVIAK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 IVETLAWFTVVASLFALPOM------RRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVL--GITCGVMVWAGIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molar, Istvan
APPLICANT: Molar, Istvan
APPLICANT: Gyr, Devon
APPLICANT: Gyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-3058A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILIO APPLICATION NUMBER: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.2%; Score 86.5; DB 1; Length 431; Best Local Similarity 27.4%; Pred. No. 0.085; Matches 49; Conservative 21; Mismatches 56; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.8%; Score 82; DB 4; Length 713; Best Local Similarity 22.0%; Pred. No. 0.55; Matches 46; Conservative 29; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               53 AGIALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSA---
    5693465 32,925
REGISTRATION NUMBER: Reg. No. 5693
REFERENCE/DOCKET NUMBER: WMM.56
TELECOMMUNICATION INFORMATION:
TELEPAX: 703/685-0573
TELETAX: 2484.25
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERICTICS:
LENGTH: 431 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-335-409-11
                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-311-023-2
                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                TYPE: ami
TOPOLOGY:
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US-09-335-409-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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      43 LGITCGV--MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGCLYLCWMGYQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NICHOLSON, Robert lan
APPLICANT: GEE, JULIA MATGAREC
APPLICANT: GREE, JULIA MATGAREC
APPLICANT: GREEN, Christopher Douglas
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: BREAST TUMOURS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 91; DB 6; Length 153
25.5%; Pred. No. 0.0064;
tive 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: TBM PC COMPATIBLE
COMPATER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY/AGRIT INFORMATION:
NAME: PATCH, Andrew J.
                                                                                                                                                           RESULT 2
5474933-4
; Patent No. 5474933
; PAPLICANT: EINER, RONALD M.; FUQUA JR., WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
HILNG DATE: 08-00x-1993
; PRIOR APPLICATION DATA:
RELING DATE: 10-NOY-1993
; PRICH APPLICATION NUMBER: 974,837
FILING DATE: 10-NOY-1992
; APPLICATION NUMBER: 496,804
; FILING DATE: 21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08311023
Patent No. 5693465
GENERAL INFORMATION:
GAPPLICANT: MANNING, David Lockwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Young & Thompson 745 South 23rd Street
                                                                                            : : | | : | : : : | | 123 POLMVLLSIIMMT-EFFSMLA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.5%
Matches 36; Conservative
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CITY: Arlington
STATE: VA
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US-08-395-246C-2
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                                                                                                                                                                                        Sequence 3, Application US/09097759A

Sequence 3, Application US/09097759A

Sequence 3, Application US/09097759A

Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, 
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Sequence 2, Application US/09097759A;
Patent No. 5972663
GENERAL INFORMATION:
APPLICANT: Winterhalter Mr., Christopher
TITLE OF INVENTION: Matroorganisms and Processes for the Fermentative
TITLE OF INVENTION: Preparation of L-cysteine,
TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
FILE REFERENCE: Minterhalter
CURRENT APPLICATION NUMBER: US/09/097,759A
CURRENT FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: DE 197 26 083
EARLIER PILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL--IMVGGGLYLCWMGYQMLR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 -- LRFMLVAFPAIFFVARPKVPL-----NLLLGYGLT-----ISFAQFAFLFCAINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80.5; DB 2; Length 299; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 25.0%; Pred. No. 0.25,
Matches 45; Conservative 27; Mismatches
| :| :| :| 1:
153 VLIERESMRRSYAQVTLAAGVVSEVAAWV 181
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US-09-097-759-3
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
LENGTH: 299
TYPE: PRT
                                                                                                                                   RESULT 5
US-09-097-759-3
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US-09-097-759-2
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LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ---WMGYQMLRGALKK-----EAVSA------PAPQVELAKSGRSFLK 117
                                                                                                                                                                                 GTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                           -----PQVELAKSGRSFLKGL-LTNLANPKAIIYFGSVFSLFVGDNV 144
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34 SRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL--IMVGGGLYLCWMGYQMLR 91
                           71;
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Peery, Robert B.
APPLICANT: Skartud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: ASPERGILLUS FLAVUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 GLLTN---LANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.5%; Score 79.5; D
Best Local Similarity 18.4%; Pred. No. 2.4;
Matches 41; Conservative 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,246C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08395246C; Patent No. 5773214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Ell Lilly and Compai
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: x9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
TELEFAX: 317-277-1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 3578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1307 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                           92 GALKKEAVSAPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 --LIMVGGGL-----YLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSF-LKGLLTNL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRK-----EAMMGVLGITCGVMVWAGIA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 ENTHMTIWLGIVYAY-----KGLLMLFGCF-----LAWETRNVSIPAL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%; Score 77; DB 3; Length 332;
21.7%; Pred. No. 0.72;
tive 31; Mismatches 69; Indels
960 PIVKSSLLYASSQALPFFCMALGFWYGGSLLGHGEYSLFQFYV 1002
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
                                                                                                   Sequence 4, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
APPLICANT: STAWNER, LISA
APPLICANT: STAWNERS, WELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPENDENCE ADDRESS:
ADDRESSE: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 LLGL--HLIIEK------MAWLHT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/09/183,253
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 846169
INFORMATION FOR SED IN 0: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%
Best Local Similarity 21.7%
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-183-253-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                       19482
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                                                                SULT 8
-09-183-253-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRK----EAMMGVLGITCGVMVWAGIA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 77; DB 3; Length 859; ilarity 21.7%; Pred. No. 2.6; Conservative 31; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 LLGL--HLIIEK------MAWLHT-----
                                                                   APPLICANT: VAWTER, LISA
APPLICANT: STAMMERS, MELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GP-70395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION NDTA:
APPLICATION NUMBER. 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestla, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/08612734B
; Patent No. 5914246
; GENERAL INFORMATION:
Sequence 2, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
                                                                                                                                                                                      ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 846169
INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-183-253-2
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
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US-08-612-734B-2
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70 -----LHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSG---RSFLKGL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 RKEAM-----WGVLGITCGVMV-----WAGIALLGLHLIIEKMAW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 RKEAIQRMLISLGIAILLIFAAFKLGAAGITLYNLIRLLVGSLAYLAIFGLLIYLFFFKW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 73.5; DB 2; Length 783; 25.3%; Pred. No. 5.8;
tive 24; Mismatches 64; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Flugge, Ulf-Ingo
APPLICANT: Weber, Andreas
APPLICANT: Fischer, Karsten
TITLE OF INVENTION: DNA MOLECULES WHICH CODE FOR A PLASTID
TITLE OF INVENTION: 2-OXOGLUTARATE/MALATE TRANSLOCATOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq c/o FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,837
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28,354
ER: GM10077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08750723A Patent No. 5981219
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Dickinson, O. Todd
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM1C
TELECHONICACTION INFORMATION:
TELEPHONE: 215,994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-922-837-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                 COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 MRRGYQRLAKWIDG 189
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COMPUTER READABLE FORM:
                                                                                        CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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US-08-750-723A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946 YMLAQFQQRSKSAYEGSASYAC------EATSAIRTVASLTREQDVWGVYHDQ 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993 LOKOGRKSLISVLRSSLLYASSQALVFFCVALGFWYGGTLLGHHEYSIFRFFV 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 LAKSGRSFLKGLLTN---LANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1349;
...rllCaNT: Peery, Robert B.
APPLICANT: Skatrud, Paul L.
APPLICANT: Tobin, Matthew B.
TITLE OF INVENTION: Multiple Drug Resistance Gene of TITLE OF INVENTION: Aspergillus Fumigatus
CORRESONDENCE ADDRESS:
ADDRESSEE: Bli 1:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ------MMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTLIMV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chalker, Alison F.
APPLICANT: Feliu, Maria M.2.
APPLICANT: Brown, James R.
APPLICANT: Brown, James R.
TITLE OF INVENTION: NO. 5888770el Spoilie
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ACCHESTORE PLICE & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,734B
FILIG DATE: 08-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%; Score 76.5; Best Local Similarity 15.9%; Pred. No. 5.9 Matches 37; Conservative 29; Mismatches
                                                                                                                                                                                                                                   ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center, DC1501 CITY: Indianapolis STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Craig, Anne I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: X-9681
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-354-4643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-922-837-2
Sequence 2, Application US/08922837
Parent No. 5888770
GENERAL INFORMATION:
APPLICANT: Chalker, Alison F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-354-4043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 1349 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 46285
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 ------KKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 GAAHIGAMFTAFLSVASALGTPPFLAAIVLSFLSNLMGGLTHYGIGSAPVFYGANY---- 534
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,723A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: DE P4 420 782.4
APTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESq.
REJESTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: GFB-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08924747
Patent No. 6063570
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: BNZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: TBM PC COMMATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION DATA:
RILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...URESSEE: E.I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAGATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 SRKEAMMGV-LGITCGVMVWAG-----IALLGLHLII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.9%; Score 73; DB 2
Best Local Similarity 20.8%; Pred. No. 4.3;
Matches 43; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 --- VPLPQWWGYGFLISIVNLIIWLGV 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 569 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-750-723A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 WMGY-----QMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 LFVGDNVG-TTARWGIFALIIVETLAWFTVVASLFALPQM-RRGYQRLAKWIDGFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 LFVGDNVG-TTARWGIFALIIVETLAWFTVVASLFALPQM-RRGYQRLAKWIDGFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09247373B

Sequence 8, Application US/09247373B

Patent No. 6168954

GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOTBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
CURRENT PILING DATE: 1099-102-10
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: MICROSOFT Office 97
TEMMEN: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 6.7%; Score 71; DB 4; Length 234; Local Similarity 25.0%; Pred. No. 2.2; hes 29; Conservative 15; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.7%; Score 71; DB 3
Best Local Similarity 25.0%; Pred. No. 2.2;
Matches 29; Conservative 15; Mismatches
                                                                     CL-1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-296-715-8
; Sequence 8, Application US/09296715
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA ARAMETHY
REGISTRATION NUMBER: 33 692
REFREENCE/DOCKET NUMBER: CL-1:
TELECHMUNICATION INFORMATION:
TELECHONE: 302-892-8112
INFORMATION FOR SEQ. ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLGGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: SE3.03B09
US-08-924-747-8
                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: SOYBEAN
US-09-247-373B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-247-373B-8
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FREERIC NO. 6171839
GERRAL INFORMATION:
GARBALL INFORMATION:
FARBALL ANTON NUMBER:
FARBALLANTON `

Search completed: May 6, 2001, 14:39:24 Job time: 415 sec



i D90824 E.coli genomic DNA, i D90823 E.coli genomic DNA, i AF188935 Bacillus anthracu i AP001519 Bacillus halodur

16-SEP-2000

PAT

Tokhmakova, I.L. and

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187. 807

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ALMYETVASLFALDQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR"

192 c 248 g 235 t
                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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2 Belareva, A.V., Aleshin, V.V., Livshits, V.A., Tok
2 akataeva, A.P.
Gene and method for producing 1-amino acids
Patent: EP 1013765-A 3 28-JUN-2000;
AJINOMOTO KK (JP)
Location/Qualifiers
1. 340
/db_xref="taxon:562"
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Gaps: 0
Percent Identity: 100.000
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8.2e-09
8.1e-08
8.7e-07
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Sequence 3 from Patent EP1013765.
AX030177
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190.00
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Ratio: 5.117
Percent Similarity: 100.000
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US-09-466-935-4 x AX030177
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LOCUS AX030177
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gb_ba1:AF188935
gb_ba2:AP001519
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
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10592 | AR0005613 Escherichia coli Oli |
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11509 | AR00046 Escherichia coli Oli |
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20457 | AR0208183 Mus musculus clone |
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2046 | AR00140 Escherichia coli Oli |
2046 | AR00140 Escherichia coli Oli |
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2047 | AR00469 Pseudomonas aeruginc |
2045 | AR00469 Pseudomonas aeruginc |
2046 | AR235020 Brucella melitensis elider |
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                                                                                                   version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2483 1
7285 1
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                                                                                             About: Results were produced by the GenCore software,
Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EScore . 5e-97 . 5e-96
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6e-08
4e-08
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Search time (sec): 1745.950000
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9b_bat; AX005613
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9b_htq17; ACC02085
9b_ba2; ECCRECO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_bal:AE004946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_ba3:U32810
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Cations"
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Strain MG1655: B3816"
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Established.

E Chases I to 10592)

Berna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J. D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A. and Blattner, F.R.
Genome sequence of enterchemorrhagic Escherichia coli 0157:H7

L. Nature 409 (6819), 529-533 (2001)

E (bases I to 10592)

E (bases I to 10592)

Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick H.A.,
Grotbeck, E.J., Davis, N.W., Lim, S., Boutin, A., Shao, Y., Miller, L.,
Robbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Welch, R.A. and Blattner, F.R.
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3 of 3, section 232 of 290.
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Escherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Submitted (22-OCT-2000) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               437 GGATGGCTTACCAGATGCTACGTGGTGCACTGAAAAAAGAGGCGGTTTCT 486
                                                                                                                                                                                                                134
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LOCUS Ab005613 10592 bp DNA
Scherichia coli 0157:H7 genome, contig
ACCESSION Ab005613 Ab005174
VERSION AB005613.1 GI:12518685
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ACCESSION
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KEYWORDS
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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to: 10592
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Percent Similarity: 100.000
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US-09-466-935-4 x AE005613
                                                                                       gene
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Strain MG1655: B3821"
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                                                                                                                                                                                                                                                                                                                                                                                                                   101 AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlyS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GlyllePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
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                                                                                                                                                                                                                                                                                                                                                             1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9307 AIGTIGATGTTATTTCTCACCGTCGCCATGGTGCACATTGTGGGCGCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 tAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysT
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Gaps: 0
Percent Identity: 100.000
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/ WLAILLY 13.30 / 0.1 
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NHDSNGFSDFTGRSWNRLYTRLMABNGNMJVFWKWYVGNTDDNPDJTRYNGYYQLK

IGYHLGDAVLSARGGYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQ

TRVYGYGYMLNDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="orf; Unknown"
/hote="0122; sequence change shortens and
changesN-terminus relative to earlier version (YIGJ_ECOLI
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/function="enzyme; Central intermediary metabolism:
Phosphorus compounds"
/note="0.289; 99 pct identical to PAI_ECOLI SW: P00631;
CGSCNO. 384"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="factor Sigma70; predicted +1 start at 4003392"
1019. .1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="o610; 99 pct identical to 607 amino acids of RECQ_ECOLI SW: P15043 but has 3 additional N-ter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="enzyme; DNA - replication, repair,
restriction/modification"
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Location/Qualifiers
1. .11509
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/gene="yigJ"
/note="b3823"
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   FEATURES
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Explainted (13-051-1699)

Direct Submission

Direct (15 Lill.

Direct Submission

Submitted (13-057-1998) Laboratory of Genetics, University of Wisconsin 445 Henry Mall, Madison, WI 53706, USA

Wisconsin 445 Henry Mall, Madison, WI 53706, USA

Wisconsin 445 Henry Mall, Madison, WI 53706, USA

Wisconsin Augusta HG00301 and HG01428 (from the Human Genome Project and NCHGRS). The entire sequence was independently determined from E. Coll KIL strain MG1655. Predicted open reading frames were determined using Genewark software, Kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with GS site Nos. unique ID nos. for the genes in the E. coli Genetic Stock Center (GGS) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.piology.yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli (http://www.genetics.wisc.edu). *** The E. coli KI2 sequence and products; all new functional assignments courtesy of Monica Riley; added promoters, wisc.edu). *** The E. coli KI2 sequence changes. Annotation updated; this is version MS4. No sequence changes. Annotation updated; this is version MS4. No sequences described in reference 1. The unique numeric identifications are periodically updated; this will genetic sequence of labels. This should allow them to be searched for in Entrez as gene names.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 11509)
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V.,
Blattner, F.R., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F.,
Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J.,
Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 11509)
Blattner, F.R.
Direct Submission
Submitted (16-7AN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli K12
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                          AE000458 11509 bp DNA BCT 01-DEC-2000 Escherichia coli K12 MG1655 section 348 of 400 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
                                                                                                                                                                                                                                                                                                                          genome.
AE000458 U00096
AE000458.1 GI:2367299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 11509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli K12.
                                      9907 CATTTGATTATTTCGCGG 9924
   201 HisLeuIleIleSerArg 206
                                                                                                                                      seq_name: gb_bal:AE000458
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                                                                                                                                                                                                           seq_documentation_block:
LOCUS AE000458
                                                                                                                                                                                                                                                                            DEFINITION
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TITLE
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KEYWORDS
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FVRRRAGHURNYVICFORTESYYKY XELAZUDFHLGFDVLT IDHGGORGGRILADD
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LTAPWFGIVIRMPSFWARQILNWAEAHPRFRDGYAIGTGRWRALPFAINVLTHSRQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRNLRFYADDPTIRVGGPTYHWVRESILAGEQVLAGAGDDATPTLLLQAEEERVVDNR
MHDRFCELRTAAGHPVEGGRPLVIKGAYHEILFEKDAMASVALHAIVDFFNRHNSPSG
                                                                                                                                 3612. 3645
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contains 1 REP sequence"
complement(3654. 4070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4200. .4230
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c/once="factor Sigma70; predicted +1 start at 4006629"
/note="factor Sigma70; predicted +1 start at 4006612"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5381. .5408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5494, .5523 ... Frances is start at 4007865"
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5526, .6041
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Phosphorus compounds"
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Gaps: 0
Percent Identity: 99.515
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                                                                                                                                                                                                                                                                                                /function="orf; Unknown"
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US-09-466-935-4 x AE000458
                                                                                                                                         repeat_region
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1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17

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Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
[ Chasea: 1 to 9114]
Daniels,D.L., Plunkett,G. III., Burland,V. and Blattner,F.R.
Daniels,D.L., Plunkett coli genome: DNA sequence of the region from 84.5 to 86.5 minutes
Science 257 (5071), 771-778 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plunkert, G. III., Burland, V., Daniels, D.L. and Blattner, F.R. Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1995
84.5 to 86.5 minutes.
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                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                             talaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysT
                                                                                                                                                                                                                                                                                                                  101 AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLy
tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS
                                                          erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCIS ECOUNS 91414 bp DNA BCT
DEFINITION E. coli genomic sequence of the region from
ACCESSION M87049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3572 CATITGALTATITCGCGG 3589
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to Mg chelatase subunit of Rhodobacter
                                                                                                                                                                                                                                                                                                           /note="CGSC No. 18010; possible pssR gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9456)
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/hote="corresponds to Mil651 (1. .341)"
3336. .3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="corresponds to V00289 (1. .402)"
3336. .12791
                                                                                                                                                                 586. .724
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comp.tement(703. .1104)
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/note="promoter matrix score of 57"
1223. 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="promoter matrix score of 63" 1151. .1179
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complement(1585. 3135)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA67568.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1136.
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Submistated (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu; Phone: 608-262-2534; Fax:
608-263-7459
On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. The entire sequence was independently determined from E. coli Mol565. Overlaps and conflicts with other sequence determinations are annotated. Reference [1] describes the original sequence determination of a 91408 by sequence. References [2], [3], and [4] describe subsequent corrections and/or updates to that sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // Organism="Escherichia coli"
// Organism="Escherichia coli"
// Strain="MG1655"
// Sub_strain="MG1655"
// Sub_strain="MG1655"
// Cone_lib="lambda library of Daniels and Blattner"
// Map="bp l at 3974 kl; M8.7 minutes"
// Note="This sequence comprises the following lambda clones: D0850(EC15-116), D0851(EC13RM4), D0854(EC15-177), D0865(EC19RM8.1), D0868(EC17RM9), D0865(EC17-221), D0866(EC17-221), D0866(EC17-280). M13Mp19 or Janus vectors were used for
                                                                                                                                                                                                            4 (bases 1 to 91414)
Rudd, K.E., Sofia, H.J., Koonin, E.V., Plunkett, G. 3rd, Lazar, S. and
Rouviere, P.E.
                                                                                                                          DNA sequence of the
                                              (bases 1 to 91414)
Blattner, F.R., Burland, V., Plunkett, G. III., Sofia, H.J. and
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                                                                                            Daniels, D. L. Analysis of the Escherichia coli genome. IV. region from 89.2 to 92.8 minutes Nucleic Acids Res. 21 (23), 5408-5417 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253. .396
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complement(266. .862)
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
93347969
                                                                                                                                                                                                                                                                                 A new family of peptidyl-prolyl isomerases
Trends Biochem. Sci. 20 (1), 12-14 (1995)
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/gene="f198"
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/note="CGSC No. 989"
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Daniels, D.L.
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Direct Submission
Submitted (09-PEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs GLIMMER (Salzberg, S., Delcher, A., Kasif, A. and White, O. (1998) NAR 26,544-548), and Genewark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,1107-1115.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, Mo 63110, USA
e-mail: sclifton@watson.wustl.edu or
jspieth@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                       61212 AGT. TTACTGACCAATCTCGCTAATCCGAAAGCGATTATCTACTTTGGCT 61260
                                                                                                                                                                                                                       The Salmonella typhimurium Genome Sequencing Center.
Unpublished
                                                                                                           erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                                                                                                                                                                                                  151 GlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa 167
                                                                                                                                                                                                                                                                                      167 lAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                       sGlyLeuLeuThrAsnLeuAlaAsnProLysAlalleIleTyrPheGlyS 134
                                                                                                                                   /organism="Salmonella typhimurium LT2"
/strain="SGSC1412"
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Locus srystmp1 96086 bp DNA
DBFINITION Salmonella typhimurium fragment STMD1.
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1 (bases 1 to 96086)
Washington University Genome
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Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mogawvvhalraogvwivegypggaimpvydalydggvehllc
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                                                                                                                                                                                                                                                                                                                                                                       /product="acetohydroxy acid synthase II, large subunit"
/protein_id="AAA67571.1"
/db_xref="GI:148175"
                                                                                                                                                                                                                                                                                                         /note="CGSC No. 603; inactive in wild-type E. coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="the mutation ilv02096 joins this ORF to ilvG, restoring function missing in wild-type"
                                                                                                                                                                                                  /translation="MTALLRVISLVVISVVVIIIPPCGAALGRGKA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 rpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSer 100
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KLDLVDAMIQGADPKVSDDQSNQVERSACPTCGSCSGMFTANSMNCLTEALGLSQPGN
GSLLATHADBKQLFLNAGKRIVELTRRYYEQNDESALPRNIASKAAFENAMTLDIAMG
GSTLATHADBKQLFLNAGKRIVELTRRYYEQNDESALPRNIASKAAFENAMTLDIAMG
GSTNTVLHLLAAAQEAEIDFWSDIDKLSRKVPQCKTVAPSTQKYHMBRDFHRAGGVLG
ILGELDRAGILINRWKNVLGTLLPOTILEQYDITTVTQDEAVKKMFRAGPAGTRETTQAFG
QDCRWDSLDDDRAAGCIRSLEYAYSKDGGLAVLYGNFAENGCIVKTAGVDDSILKFTG
PARVYESQDDAVBAILGGKVVBGDVVVIRYEGPRGFGMQBMLYPTGFLKSWGLGKAC
ALITGGRFSGGTSGLSIGHVSPEAASGGTIALIEDGDTIAIDIPNRSIQLGSEAEIA
ARREAGERAGDKAWTPKNRQRQVSFALRAYASLATSADKGAVRDKSKLGG"
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seq\_name: gb\_htg16:AC073768

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Summary Statistics
Consensus quality: 230709 bases at least Q40
Consensus quality: 258916 bases at least Q30
Consensus quality: 258916 bases at least Q30
Consensus quality: 258916 bases at least Q20
Estimated insert size: 216600; agarcse-fp estimation
Estimated insert size: 216600; agarcse-fp estimation
Quality coverage: 9.54 in Q20 bases; agarcse-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Unpublished
J. (bases 1 to 279589)
Dor Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 10 (bases 1 to 279589)
DOE Joint Genome Institute.
                                               29-JUN-2000
seq_documentation_block:
LOCUS AC073768 279589 bp DNA HTG 29-JUN-20
DEFINITION MUS musculus clone RP23-359N18, WORKING DRAFT SEQUENCE, 60
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1109: gap of unknown length
2123: contig of 1023 bp in length
2123: gap of unknown length
3357: contig of 1025 bp in length
4550: contig of 1193 bp in length
4550: contig of 1193 bp in length
4450: contig of 1194 bp in length
6514: contig of 1164 bp in length
6514: gap of unknown length
7557: contig of 1043 bp in length
7557: contig of 1043 bp in length
8885: contig of 1028 bp in length
1056: contig of 1228 bp in length
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Web site: http://www.jgi.doe.gov
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Gaps: 4
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    seq_documentation_block:
    LOCGS
    AC020885
    268294 bp
    DNA
    HTG
    16-FEB-2000

    DEFINITION
    Mus_musculus
    Clone RP23-46411, LOW-PASS
    SEQUENCE SAMPLING:

    ACCESSION
    AC020885
    AC020885.2
    G1:6980212

    KEYWORDS
    HTG; HTGS_PHASEO.

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Percent Identity: 96.602
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                 110431
                                                                 Quality:
                                                                                           Percent Similarity:
                                                                               Ratio
                                                  alignment_scores:
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| * 15873 16608: contig of 736 bp in length  * 16609 16851: contig of 243 bp in length  * 16852 17277: contig of 426 bp in length  * 17278 18057: contig of 426 bp in length  * 17278 18057: contig of 780 bp in length  * 18058 18704: contig of 647 bp in length  * 18705 19414: contig of e47 bp in length  * 18705 19414: contig of in length  * 18705 19414: contig of in length  * 18705 19414: contig of 100 bp in length  * 18705 19414: contig of 100 bp in length  * 18705 19414: contig of 100 bp in length | 21010: contig<br>21258: contig<br>23639: contig<br>24853: contig<br>24853: contig<br>25795: contig<br>27729: contig<br>27729: contig<br>27729: contig<br>29714: contig<br>29714: contig<br>33791: contig<br>33791: contig<br>33791: contig<br>33791: contig<br>34848: contig<br>35602: contig<br>35602: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig<br>38059: contig | * 41689 42688: contig of 1000 bp in length<br>* 42689 43847: contig of 1159 bp in length<br>* 43848 44511: contig of 664 bp in length                                             |
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| SOURCE<br>ORGANISM<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOHNAL<br>AUTHORS<br>TITLE<br>JOHNAL                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                   |

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| gap of unknown length age of unknown length age of unknown length gap of unknown length gap of unknown length gap of unknown length agap of unknown length less; contig of 1005 bp in length agap of unknown length gap of unknown length | Length: Gaps: Percent Identity: 98 frw f: AC020885 from: 1 t eurleMetValGlyGlyLeu [                                                                                             |
| 1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | alignment_scores:  Ouality: 717.00 Ratio: 5.158 Ratio: 5.158 alignment_block: US-09-466-935-4 x ACO20885/. Align seg 1/1 to reverse o 67 MetalaTrpLeuHisThrL. 11743 STTPMEGGIJI |

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Culpublished

2. (basses 1 to 290452)

Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R.,

Grodin, M., Goltz, J.S. and Kucherlapati, R.

Grodin, M., Goltz, J.S. and Kucherlapati, R.

Direct Submission

Submitted (23-AuG-2000) Department of Molecular Genetics, Albert

Binstein College of Medicine Genome Center, 1300 Morris Park Ave.,

Bronx, NY 10461, USA

On Aug 30, 2000 this sequence version replaced gi:9885883.

Albert Einstein College of Medicine Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29045); Montgomery, K. T., Lee, E., Long, J., Pomerantz, R., Grille, G., Han, J., Montgomery, K. T., Lee, E., Long, J., Pomerantz, R., Gordon, M., Goltz, J.S. and Kucherlapati, R., High, Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                           ** NOTE: This is a 'working draft' sequence. It currently strong the 196 configs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                      166
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AC079167.2 GI:9945047
HTG; HTGS_PHASE1.
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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AUTHORS
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JOURNAL
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| et.                                                                                 |                     |                |                     |                                       |                |           |         |           |                                      |         |           |         |                 |        |             |        |                |             |        |              |                                   |        |                |                                   |                  |                |                                   |        |        |              |                 |                  |              |                                   |        |                |        |                 |                                   |        |                 |                                       |        |                 |                |             |                 |                  |        |
| h the finished sequence<br>the accession number will<br>2 bp in length<br>wn length | enoth               |                | ength               | րու                                   | , and c. i     | in length | •       | in length | ուցա<br>in length                    | 11.6    | in length | •       | in Length       | enath  |             | length | ,<br>1         | in fina     | ength  |              | .engtn                            | length | 1 4 1 1        | reng cn<br>h                      | ength            | 14.1           | engru                             | ength  | onot b |              | ength           | ength            | 44.4         | tengtn                            | length | on at h        | angen  | length          | anath                             |        | ength           | n<br>Jenath                           |        | length          | n<br>Jenath    |             | length          | ength            | :: 6:: |
| d with the fini<br>and the access<br>of 852 bp in le<br>unknown length              | of 881 bp in length | unknown length | of 885 bp in length | unknown length<br>of 836 bp in length | unknown length | Q,        | nown le | δ.,       | on Ribwii Tenguni<br>of 869 hp in 16 | nown le | Q         | nown le | ot 866 bp in Le | renger | nown length | ni qq  | unknown length | nown length | p in 1 | snown length | or 85/ ap in le<br>unknown length | p in   | unknown length | or 923 op in le<br>unknown lenath | of 946 bp in ler | unknown length | oi /93 op in le<br>unknown length | p in 1 | ngth   | cnown length | of 852 bp in le | rengul<br>p in 1 | cnown length | or 1240 op in J<br>unknown length | p in   | unknown length |        | of 920 bp in le | unknown length<br>of 812 bp in le | cnown  | of 940 bp in le | unknown Lengtn<br>of 866 bp in length | cnown  | of 893 bp in le | Lengt<br>op in | known lengt | of 851 bp in le |                  | 9      |
| <pre>pdate railable contig gap of</pre>                                             |                     |                |                     |                                       | dap of         |           |         | 1.g       |                                      |         | contig    |         | 91,0            | contia |             |        |                | <b>л</b> чч |        | gap of       | contig<br>dan of                  | contig | <b>u</b>       | gap of                            | cig              | <b>u</b>       | gap of                            | ijg    | gap of | gap of       | contig          | 119              |              | gan of                            |        | gap of         | gap of |                 | gap of                            | gap of | contig          | gap or                                | gap of | contig          | gap or         | gap of      |                 | gap or<br>contiq | ۰,     |
| i will be<br>it is av<br>ed.<br>852:<br>872:                                        |                     |                |                     |                                       | 3534:          |           |         |           |                                      | 6293:   | 7095;     | 7115:   | 7981:           | 8729:  | 8749:       | 9875:  | 9895:          | 10651:      | 11577: | 11597:       | 12474:                            | 13334: | 13354:         | 14299:                            | 15245:           | 15265:         | 16078:                            | 16945: | 16965: | 17870:       | 18722:          | 19556:           | 19576:       | 20836:                            | 21756: | 21776:         | 22537: | 23457:          | 23477:                            | 24309: | 25249:          | 25269:                                | 26155: | 27048:          | 28003:         | 28023:      | 28874:          | 29777:           |        |
| 4 5 1                                                                               | 873                 | 1754           | 1774                | 2639                                  | 3515           | 3535      | 4450    | 44/0      | 5405                                 | 6274    | 6294      | 7096    | 7116            | 8002   | 8730        | 8750   | 9876           | 10632       | 10652  | 11578        | 12455                             | 12475  | 13335          | 14280                             | 14300            | 15246          | 16059                             | 16079  | 16946  | 17851        | 17871           | 18743            | 19557        | 20817                             | 20837  | 21757          | 22518  | 22538           | 23458                             | 24290  | 24310           | 25270                                 | 26136  | 26156           | 27069          | 28004       | 28024           | 28895            | 1 1 1  |
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                                                                                                                                                                                                                                 /gene="reco"
479. 2311
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4.629
98.131
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Ratio:
Percent Similarity:
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ORIGIN
                                                                                                                                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli (strain K-12) DNA.
Escherichia coli
Escherichia coli
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 2695)
Irino,N., Nakayama,K. and Nakayama,H.
The reco gene of Escherichia coli K12: Primary structure and evidence for SOS regulation
Mol. Gen. Genet. 205, 298-304 (1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 GlyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIl 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 uLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
f unknown length
g of 873 bp in length
f unknown length
g of 851 bp in length
f unknown length
g of 1051 bp in length
f unknown length
                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 99.138
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1. .352
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61879:
62752:
62772:
63623:
63643:
64694:
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US-09-466-935-4 x AC079167
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LOCUS ECORECO
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   61860
61880
62753
62773
63624
63644
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AUTHORS
TITLE
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/ vullel- old tide. "MY ADAR THE SCAROVLOETE GYOOF REGOED ID TY LISTA AT 10.0."

/ trains lation= "MAYOAEVLINGLY VVSPLISLMK DOYDOLOANG VAAACLNSTOT REQOLE VARGEOFF REQUIRE AT 10.0."

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                                                                                                                                                                                    /translation-"SWNRLYTRLMAENGNWLVEVKPWYVGNTDDNPDITKYMGYYQL
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479. ,2311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMe 67
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Percent Identity: 98.131
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                                               | 17938: contig<br>17938: contig<br>gap of<br>18715: contig<br>19493: contig<br>gap of | 20780:<br>21499:<br>21570:<br>22378: | 23943: contig<br>24650: contig<br>24650: contig<br>3ap of<br>35686: contig                                                                                                                                                                                                         | * 25687 25820: contig of 134 bp in length  * 25821 26268: contig of 448 bp in length  * 26269 27152: contig of 848 bp in length | * 27153 28057: contig of 905 bp in length  * 28058 29002: contig of 945 bp in length  * 28058 29002: contig of 945 bp in length  * 29003 29991: contig of 989 bp in length                                     | 30780: contigo                                                                                                                           |                                                                                                                                                                                                                                                      | 37013:<br>38147:<br>38852:<br>39840:<br>40874:<br>42387:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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| LOCUS  AC020833 62274 bp DNA HTG 16-FEB-2000  DEFINITION MUS MUSCULUS CLONE RG-WBAC_40H2, LOW-PASS SEQUENCE SAMPLING. ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSIO |                                                                                      |                                      | * However, it should not be assumed that this clone  * will be sequenced to completion. In the event that  * the record is updated, the accession number will  * be preserved.  * 296: contig of 296 bp in length  * app of unknown length  * 207: 10.00 contig of 25 bp in length | 1812: Concig<br>1812: Contig<br>gap of<br>2420: Contig                                                                          | * 2421 293: CONTIGO TO 33 DP IN LENGTH  * 2954 3645: CONTIGO OF 692 DP IN length  * 3646 4766: CONTIGO Of 121 DP IN length  * 3646 4766: CONTIGO Of 121 DP IN length  * 4767 5206; CONTIGO Of 121 DP IN length | 5584: CONLIG OL 330 DJ<br>gap of unknown<br>5584: CONTIG Of 288 DJ<br>gap of unknown<br>6454: CONTIG Of 870 DJ<br>6853: CONTIG Of 399 DJ | * 6854 7566; contig of 713 bp in length  * 7567 8253; contig of 687 bp in length  * 8254 9058; contig of 687 bp in length  * 8254 9058; contig of 805 bp in length  * 9059 9678; contig of 600 bp in length  * 9059 9678; contig of 600 bp in length | of 594 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property of 148 by the property |

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complement(3294. 3938)
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May,B.J., Zhang,Q., Li,L., Paustian,M.L., Whittam,T.S. and Kapur,V.S.
Complete nucleotide sequence of an avian isolate of Pasteurella
                                                                                               Proc. Natl. Acad. Sci. U.S.A. (2001) In press
2 (Dases 1 to 10184)
2 Shang O. and Kapur, V.
Direct Submission
Submitted (24-0CT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 10184
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/gene="dapB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3294. .3938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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105. .1820
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1814. .2392
                                                                                                                                                                                                                                                                                                                                                                                                                 105. .1820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="dapB'
                                                                                   multocida
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                                                                                                     JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                      TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                           FEATURES
                                                      TITLE
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Pasteurella multocida
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
1 (bases 1 to 10184)
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Pasteurella multocida PM70 section 77 of 204 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 nValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 others
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length
'n length
                            bp in length
length
bp in length
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bp in length
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bp in length
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10653 GTTATTTGCCGGATTTGCCATTCATTTGATTATTTCGCGG 10614
                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                       length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 aLeuPheAlaGlyPheGlyIleHisLeuIleIleSerArg 206
                                                                                                     qap of unknown is contig of 1434 by contig of 1434 by eap of unknown is 48115: contig of 1007 by gap of unknown is 1661: contig of 1756 by gap of unknown is 51661: contig of 1790 by gap of unknown is 53728: contig of 2067 by 5978: contig of 3056 by gap of unknown is 59220: contig of 3056 by gap of unknown is 59220: contig of 3056 by gap of unknown is 62274: contig of 3054 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 0.6274 ". 0.6274"
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/ Ab xref="taxon:10090"
/ Clone="RG-WBAC_40H2"
16965 a 13547 c 13251 g 18170 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to reverse of: AC020833 from: 1
                                                         unknown
of 1309
     gap of
contig
gap of
                                                                                   contig
gap of
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AE006110 AE004439
AE006110.1 GI:12721018
                               44365:
                                                                                45674:
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US-09-466-935-4 x AC020833/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
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LOCUS AE006110
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                            43259
                                                                                                                               45675
                                                                                                                                                                                   47109
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                                                                                44366
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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                                                                                                                                                                                   algyagomftfyglulpvgmamrarkrypdlpyrvmggnltlfgalilgilimnvpfl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3938 GIGATGTTAAATCTTATTGTACATTTTTTCGGTTTAATCACGCCAGG 3889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3888 ACCCGACTITITITATGTCAGTCGATTAGCTGCCAGTAATTCACGTCGTA 3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yProAspPhePheValSerGlnThrAlaValSerArgLysG
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Gaps: 2
Percent Identity: 37.073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown"
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75.122
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Percent Similarity:
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white,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.

Direct Submission

Direct Submission

Submitted (27-SEP-1997) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
corresponding H. influenzae genes

S. (hasse 1 to 1137)

White,O. Clayton,R.A. Kerlavage,A.R., Fleischmann,R.D.,
Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.

Direct Submission

N. Submitted (28-MAY-1998) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

The whole genome was shifted by 588 nucleotides for a new start

On oct 1, 1996 this sequence version replaced gi:1222062.

Location/Qualifiers

Ince
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Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A.,

Kelley,J.M., Weidman,J.F., Phillips,R., Liu,L.I., Glodek,A.,

Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,

Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M.,

Geoghagen,N.S., Gnebm,C., Fritchman,J.L., Fuhrmann,J.L.,

Geoghagen,N.S., Gnebm,C.T., McDonald,L.A., Small,K.V., Fraser,C.M.,
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Metabolism and evolution of Haemophilus influenzae deduced from Whole-genome comparison with Escherichia coli
Curr. Biol. 6 (3), 279-291 (1996)
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Haemophilus influenzae Rd section 125 of 163 of the complete
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Raemophilus.
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White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
Direct Submission
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                                                                                                                        3688 ACCTTATGTTAAAAAGT.....CAACAAAATGTGGTTTTCGAGCCAGTT 3645
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                                                87 yrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAla 103
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4144 GITGTGATGCTAAATITAATCATTGTGCATTTATTTGGATTAATGACGCC 4193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4629 ITITIATGIGALTICATIGATTITITICACGIAATATIGCCAAGCGITTAT 4678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4194 AGGGCCTGATTTCTTTTATGTAAGTCGAATGGCGGCAAGTAACTCTCGTC 4243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4294 GGAATGCTTTCTATGTTGGGATTGGCGTGTTGTTCGTTACCATTCCAGC 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4394 GITITITAATGCCTCGCAGT.....AAAAAATACGCTAAATTTGAATCG 4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaPro 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 AlaProGlnValGluLeuAlaLysSer......GlyArgSerPheLe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 uLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 lySerValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 TrpGlyIle.....PheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 pPheThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 yrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAla 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 ysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrp 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 pLeuHisThrLeulleMetValGlyGlyGlyLeuTyrLeuCysTrpMetG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368.50 Length: 207
2.457 Gaps: 4
72.464 Percent Identity: 38.647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 11137
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5876. .6637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: U32810 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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ACCESSION VERSION KEYWORDS SOURCE REFERENCE

AUTHORS

JOURNAL

TITLE

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Vibrio cholerae

Vibrio cholerae

Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

1 (bases 1 to 11321)

Heidelberg, J.F., Elsen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.

Nierman, W.C. and White, O.

DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVANSEGPÕLHTHSVPKOVVKEADGSLTLHLENGGTYNVDTLIMAIGRHPATDAINL
AATGVATHNEGSTKINDERDINNAGSTEURIPAVAKARGOLSERLENNK
LINKKMYQÜLVPTYVFSIRP IGTIGEPQAAQAGANKVKYSKSETAMYTANTSHRO
PCKMKLVCAGPEETVVGLHGIGFAVDEMIQGFGVAMKMGATKADFDSVVAIHPTGSEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P06715 GB:M13141 PID:146248
PID:466637 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                                                                                                                        /strain="Nu6961"
/strain="Nu6961"
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/db_xef="taxon:666"
/db_cxef="taxon:666"
/chromosome="1"
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complement(69, .1433)
/gene="VC0186"
/gene="VC0186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406 (6795), 477-483 (2000)
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complement(1527. .2366)
                                                                                                                                          4729 TTTTTTGGTTGTGTGCTTGTT 4749
                                                                                          197 GlyPheGlyIleHisLeuIle 203
                                                                                                                                                                                                                                                                                                                                                                                                                           AE004109 AE003852
AE004109.1 GI:9654590
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                                                                                                                                                                                                                             seq_name: gb_bal:AE004109
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REFERENCE
AUTHORS
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JOURNAL
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gene

FEATURES

CDS

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1 (sites)
Makabone,K., Hirama,C., Takaki,Y., Masui,N., Fuji,F.,
Nakamura,Y. and Inoue,A.
An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (sites)
Takami,H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y.,
Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.
Sequencing of three lambda clones from the genome of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 eThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrG 181
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Bacillus/Staphylococcus group; Bacillus.
                                                                            8351 CCCGGGCCTGATGTCGCCTTAGTGGTGCAAAACGCTACACAGCACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8101 CCGACGCACACCCTGCGCCTCCATT...CTCGGCAACCGCCGTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LeumetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSe
                                                                                                                                           18 rProGlyProAspPhePhePheValSerGlnThrAlaValSerArgSerA
                                                                                                                                                                                                                                       35 rgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetVal
                                                                                                                                                                                                                                                                                                                                  52 TrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAl
                                                                                                                                                                                                                                                                                                                                                                             8251 CATTTGATTTTGAGCCTGTCCGGCATTAGCTACTTAGTCAAACAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                           68 aTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ......AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 rPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 yrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 AlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
Locus AP001517 294250 bp DNA
DEFINITION Bacillus halodurans genomic DNA, section 11/14.
ACCESSION AP001517 BA000004
     to: 11321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 InArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPhe 195
  to reverse of: AE004109 from: 1
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Bacillus halodurans
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VERSION
KEYWORDS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MYSMDTVNYRPSAYPAISLIEADYRQFAFERHYHLDIHIGLITQ
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RRLELEQAMKLLQSGRPGTDVAXQVGFYDQAHFSKAFKATYGLSPSLITRFS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="gamma=glutamyltranspeptidase"
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LVGLSLTWFSCLAWLLTTSAMQRMQRTRSVDSICAAVFILAGSYILMOASRALAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTYQVKQRAPVCAAYQSYQVCGMGLPSSGGLTVGQILALTEQYDLKGWGAQDVKSWQV
LGDASQLAFADRGLYMADQDYPVPTQGLLDKTYLABRAKLIQPGKALTSAPAGNPPW
HRQLRSPDQSIELLPSTSHRIVDVPREGNVVSFTTSIENAFGSRLLVFFLLNNELTDF
SFATYCSEGRPIARLEPGKRRPSSMAPTIVLODNOPYLATGSPGGSRITGYVAQAIVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:AL123456; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MMGRVCPSFFTRTSFFPPTRRGTDHFLQDKL"
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Percent Identity: 31.313
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                                                                                                                                                                                                                                                                                                                                /gene="VC0192"
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                                                                                                                                                                                                                                                                                                         complement(8485, .9297)
complement(7742. .8410)
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2798 c 3044 g 27
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                                                                       /codon_start=1
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US-09-466-935-4 x AE004109/rev
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74.747
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Quality:
Ratio:
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ORIGIN
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CDS
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GRHDLTNGLIRILHSQSFIDDPTRLLEGVRFVSFEVKFEGKTANLALATQPALTNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANVSPERIVHELKLICHETDEVSSERILEDIHVWQALIGITESSSATHLSRLOEEQN
GEPLHWFQAIATVGFLEDNWKASLVPFAITAMEQRFLONIEDIQKRLTNMTRFSTOYL
HKQLYQVPEEPLRFYALSSGEEMQKYLDLYLHQRKQLQPLLTGHDLMELGMKPSPLFR
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Complement (3074 . .4309)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKPSNNFVLSYERYKQYLKELKQVFKSFYFHEKELYHTLQAIGTNKEELISQTCTLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mnrrvvvTgIGAVTPLGNTAEETWEKAIAGQSGVGLLTRVEAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPFDANRDGFVMGEGSGILILESLESAEKRGAKIYAEIVGYGATGDAYHVTQPAPEGE
GAARAMKQAIEDAGLTPEDIQYMNAHGTSTYYNDKYETLAAKQVFGDHVNNLAISSTK
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SVLEKAGLSKEDPDFIJPHQANIRINEASRERLELPVEKMSTTVKKYGNTSSASIPMA
MVDELKDGKIKDGDLLVLVGFGAGLVWGSLALRNGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="3-oxoacyl-(acyl-carrier protein) synthase"
/protein_id="BAB06601.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown conserved protein in others"
                           /transl_table=11
/product="spore cortex-lytic enzyme"
/protein_id="BAB06598.1"
/db_xref="G1:10175501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement 3074. .4309)
/gene="BH2882"
/codon_start=1
/transl_table=11
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/gene="BH2883"
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                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                      955. .1605
/gene="BH2880"
955. .1605
/gene="BH2880"
/note="BH2880
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/gene="BH2881"
1694. .2977
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/note="BH2881
                                                                                                                                                                                                                                                                                                                                                                      unknown"
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Makasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T.,
Hirama, C., Fuji, F. and Takami, H.
Characterization and comparative study of the rrn operons of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 (bases 1 to 294250)
12 (bases 1 to 294250)
Direct Submission
Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Stechnology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
(E-mall:takamih@jamstec.go.jp,
URL:http://www.lamstec.go.jp,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
                                                                                                                                                     Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (sites)
Takani, H. and Horikoshi, K.
Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28, 4317-4331 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 (sites)
Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,
Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Hortkoshi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome analysis of facultatively alkalihilic Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g (sites)
Takami,H. and Horikoshi,K.
Analysis of the genome of an alkaliphilic Bacillus strain from industrial point of view
Extremophiles 4 (2), 99-108 (2000)
                                                                                                                                                                                                                                                                                Takami, H., Masui, N., Nakasone, K. and Horikoshi, K. Replication origin region of the chromosome of alkaliphilic Recillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
99356711
                                                                                                                                                                                                                                                                                                                                                                                                               5 (sites)
Takani, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G.,
Sasaki, R., Hirama, C., Fuji, F. and Masui, N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
                                                                                                   , Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extremophiles in deep-sea environments (Ed.);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extremophiles 3 (3), 227-233 (1999)
Bacillus sp. strain C-125
Extremophiles 3 (1), 29-34 (1999)
99184646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HORIKOSHI, K. TSUJII;
249-284; Springer-Verlag (1999)
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/gene="BH2879"
                                                                          3 (sites)
Takami, H., T
                                                                                                                                  Horikoshi, K.
                                                                                                                                                                                                                                                               (sites)
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Takami,H.
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complement(6226. .6555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52163 TTGGTATCCTAACTTCTTTAGGGATTGCTTCTGCCCTAATCGTTCATATT 52212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52263 TTTTTTACGATTCAACTATTAGGAGCTGCTTATTTAATTTGGTTAGGT 52312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 ProAlaProGlnValGluLeuAlaLysSerGlyArgSer...... 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 yrGlnMetLeuArgGlyAla.....LeuLysLysGluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 yProAspPhePheValSerGlnThrAlaValSerArgSerArgLysG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTrpLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52213 ACATALACAGTACTGGATTTGCTTTTTAATTGAAACATATCCTGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 luAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292.00 Length: 207
2.147 Gaps: 2
65.700 Percent Identity: 32.367
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                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB06605.1"
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                                                                                                                                                                                                                                                                                 complement(5903. .6157)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6226. .6555)
/gene="BH2886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AP001517 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                    'transl_table=11
                                                      5508. .5807
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                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="BH2886"
                                                                                                                                                                                                                                                                                                                            note="BH2885
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US-09-466-935-4 x AP001517
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Percent Similarity:
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Mon May 7 11:08:15 2001

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Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
        1.96
13.85
20.69
2.91
2.91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aleshin VV, Belareva AV, Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates The accumulated amino acids can then be removed from the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterium of the present invention may also be used to synthesise pmoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the L-threonine resistance gene, rhtC, from
      150.33
135.07
131.94
147.25
        81.00
81.00
80.50
80.00
80.00
                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48443
                                                                                                                                                                                                                                                                                L-threonine synthesis; rhtC;
L-leucine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 840 BP; 165 A; 192 C; 248 G; 235 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 206
Gaps: 0
Percent Identity: 100.000
                     + +
     /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:C76432
/SIDS2/gcgdata/geneseq/geneseqn/NA1001.DAT:F44668
/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:V52152
/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:212312
/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:212313
                                                                                                                                                                                                                                               coli L-threonine resistance gene, rhtC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to:
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
187..807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Page 14-15; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              /product= "RhtC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0125406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98RU-0123511.
                                                                                                                                  _documentation_block:
A48443 standard; DNA; 840
                                                                                                                                                                                                                 08-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                L-threonine resistance;
                                                                                                                                                                                                                                                                                               L-homoserine; L-valine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.117
Percent Similarity: 100.000
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US-09-466-935-4 x A48443
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P-PSDB; Y99598.
                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1013765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:T87858
/SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:T94571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseg/genesegn/NN1997. DAT: Y74475
/SIDS2/gcgdata/geneseg/genesegn/NN1997. DAT: V74486
/SIDS2/gcgdata/geneseg/genesegn/NN1999. DAT: Z12314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:C50050
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z55887
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/SIDS2/gcgdata/geneseq/geneseqn/NA2000 DAT:045934
/SIDS2/gcgdata/geneseq/geneseqn/NA1999 DAT:x06875
OM of: US-09-466-935-4 to: N_Geneseq_0401:*
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Database: N_Geneseq_0401:*
Database sequences: 678276
Database length: 291890651
Search time (sec): 172.640000
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Query: US-09-466-935-4
                                                                                                            Command line parameters:
                                 3:43
                               Date: May 6, 2001
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EP1016710-A2

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production; excretion protein gene;
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                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                              lAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                                         84
                              34
        187 ATGITGATGITATITCTCACCGTCGCCATGGTGCACAITGIGGCGCTIAI
                                                                                                                                  sGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlyS
                                                                                                                                                                                                                            erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp
                                                                                                                                                                                                                                                                  1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe
                                      237 GAGCCCCGGTCCCCGATTCTTTTTTTTCTCTCAGACCGCTGTCAGTCGTT
                                                                                                                         tAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysT
                                                                                                                                                                                                                                                                                 GlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa
                              17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS
                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Yahn"
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amino acid excretion protein; d
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/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli yahN gene
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ID A52688 standard; DNA;
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The present sequence is the yahN gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                          of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
                                                                                                                                                                                                             Ψ;
                                                                                                                                                                                                             Nakanishi K, Aleshin VV, Troshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 CAGGGGTGCTGACCGGGCTGGGCGTGGGCGTGCGTTTTATTCC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 yrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 CCGCAAATGAGCACACTACAACGAATTAGCGCCCCCTGGTATGTCTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 yProAspPhePheValSerGlnThrAlaValSerArgSerArgLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 lualaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GGGTTGGTTTGTTTGGTCTTGCAACGCTAATTACGCAGTGTGAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
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Gaps: 3
Percent Identity: 28.155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlnValGluLeuAlaLysSerGlyArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17-18; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1 to:
                                                                                          98RU-0124016.
99RU-0104431.
                                          99EP-0125263
                                                                                                                                                                                                             Zakataeva NP,
                                                                                                                                                                   (AJIN ) AJINOMOTO CO INC
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1.937
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increasing
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P-PSDB; B01786.
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                         Tokhmakova IL;
                                             17-DEC-1999;
                                                                                            30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                Livshits VA,
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05-JUL-2000
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115 .PheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleT 131

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the gene are transfected into a bacterium. The bacterium used is E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 TAGCGTCAGTAGCGGTATGAAAGCGGGTTATCTTGCGGCCTGCGGTGTAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 rgGlyAlaLeuLysLysGluAlaValSerAlaProAlaProGlnValGlu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 TAC.....GGTGCTATTTTAAACGCGCGTTAATTTTGAGCCTGAC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 aAsnProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 lyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIlelle 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 ValGluThrLeuAlaTrp.....pheThrValVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 lalaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                                                                                                                                                                                                                                                                                                                           13 IleValAlaLeuMetSerProGlyProAspPhePhePheValSerGlnTh 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 hrCysGly......valMetValTrpAlaGlyIleAlaLeu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 ACGCGACCCTGAAGGTAAAATAGCGAGGCCAAATCCGATGAGCCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 ATGTTAATGCCCCACATACG.......GGAATTTCATTCTTTATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 rAlaValSerArgSerArgLysGluAlaMetMetGlyValLeuGlyIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 LeuGlyLeufisLeuIleIleGluLysMetAlaTrpLeufisThrLeuIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 TTA.....ATTAAGACCACCCCGATATTATTCAACATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 eMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 GCGGCGACGCTGGAACTGGTGTTTCTGCTATTTGAGCTTCCTGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A61501
                                                   Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                         Gaps: 6
Percent Identity: 28.218
                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                             to: 639
                                                                                                                                                                                                                                                                                                                             from: 1
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ID A61501 standard; DNA; 1668 BP.
                                                                                                                                                 190.00
1.624
57.921
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: A52689
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US-09-466-935-4 x A52689
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                616 CGACTG 621
                                                                                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli; yeas gene; amino acid production; excretion protein gene;
  181
                                                                                                                                                                                                                                                                                                                                                                                                                              581 GGCGTATGCAACGCGTTGCCAGTCGGGTTATTGGTGCAATTATTGGTGTA 630
                                                                              131 yrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThrThr 147
                                                                                                                                                                                                                                                                                                                                                                           181 lnArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGly 197
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                                                                                                                                                                                                         AlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPh
                                                                                                                                                                                                                                                                             eThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrG
                                                                                                                                                                                                                                                                                                                          531 AGTTTTTCTTAGTCAGGCGTTTTCTTTGCCCGCTGTGCGTCGTGGTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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99RU-0104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 PheGlyIleHisLeuIle 203
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ID A52689 standard; DNA; 639
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09-MAR-1999;
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protein -
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468

427

pPhePhePalSerGlnThrAlaValSerArgSerArgLysGluAlaM

22

Mon May

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Sequences A61501-A61524 represent nucleotide sequences encoding
Agrobacterium vitis hypersensitivity response (HR) elicitor proteins
(B1630-B1688). The HR is a rapid, localised necrosis that is
(B1630-B1688). The HR is a rapid, localised necrosis that is
cubically second to be a rapid and element of the pathogenic organism interacts with a nonhost plant (i.e., one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in alling-off and killing of the pathogen. On grape plants, the A. vitis HR elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistence. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistence to disease, such as those caused by fundy, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to cold, and to impart resistence to environmental stresses, e.g., cold, and to impart nesistence to environmental stresses, e.g., cold, and to impart nesistence to environmental stresses, e.g., cold, and to impart per encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and encodes and encodes provide systemic treatment; and encodes and eliminate the need for biological control agents or polluting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of a hypersensitive response

    A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:6.

                                                                                                                                                 Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant; ds.
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Gaps: 5
Percent Identity: 27.000
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P-PSDB; B11630, B11631, B11632, B11633, B11634.
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(first entry)
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US-09-466-935-4 x A61501/rev
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23-OCT-2000
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A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:11.
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                                                                                                                                                                                                                      502 TATCATCAAATTCGTCGGCGCGCCTATCTGGTCTATGCGGCC..... 460
                                                                                                                                                                                                                                                      etLeuArgGlyAlaLeuLysLys.......GluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                          yLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerV 135
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273 TGGGGCCTGTTC.....ATCTCCCTGTCGCATTTGCTGTGGTTCGCATC
652 TITIGCCATGGTGGCGCAATAGTTTTCTTTATGGCCGCAAATCCGGGC
                                     etMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaGlyIle
                                                                                                            AlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLeuHisTh
                                                                                                                                      72 rLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnM
                                                                                                                                                                                                                                                                                                                                   ProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 TCTACACGCAATTCATCGCCAAGGACACGCCGCTGTCTCACCAATTGCTT
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                                                                                                                                             New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences A61501-A61524 represent nucleotide sequences encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1210 ..TIGGCCACGCCTTCAGCAAGATACGCGATGTCGAAGGCAGTCTGGTT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 etLeuArgGlyAlaLeuLysLys.......GluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 ProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LeuThrValAlaMetValHisIleValAlaLeuMetSerProGlyProAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 pPhePhePalSerGlnThrAlaValSerArgSerArgLysGluAlaM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 etMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 rLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLeuHisTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1668 BP; 342 A; 462 C; 423 G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 200
Gaps: 5
Percent Identity: 27.000
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WPI; 2000-376567/32.
P-PSDB; B11635, B11636, B11637, B11638.
                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 86-87; 157pp; English.
                                                                                                                                                                                                                                                  hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.471
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Ratio: 1.471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-466-935-4 x A61502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
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Novel RhtB protein, useful for generation of L-homoserine resistance in Escherichia bacteria and large-scale production of e.g. L-homoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a //*tag= a //note= "a DNA sequence corresponding to the coding region (minus the stop codon) is specifically claimed in Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1539
                                                                1296 TATTCTGACCAATGGTCTCAATCCGAAGACGTCGATTTTCGTGATCAGTC 1345
                                                                                                                                                                      1396 TGGGGCCTGTTC.....ATCTCCCTGTCGCATTTGCTGTGGTTCGCATC 1439
118 yLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerV 135
                                                                                                                                                                                                                                                                                                                                                                                   166 lValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homoserine resistance; rhtB gene; L-homoserine; L-alanine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zakataeva NP, Aleoshin VV, Belareova AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 alPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArg.....
                                                                                                                                                                                                                                                           TrpGly11ePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                1440 CGTTTCGACCTTTTTGTCCAACCGGCCATTCGAACCGTCGTGCTGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 eualaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT: 294405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli rhtB gene imparting homoserine resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-isoleucine; L-valine; L-threonine; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 10-11; 14pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294405 standard; DNA; 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-273530/24.
P-PSDB; Y79298.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1999;
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copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an amino acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of L-homoserine, L-alanine, L-isoleucine, L-valine or L-threonine (all claimed).
  amplifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ThralaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyAr 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 MetValHisIleValAlaLeuMetSerProGlyProAspPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1SerGlnThrAlaValSerArgSerArgLysGluAlaMetMetGlyValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 euGlyIleThrCysGlyVal.....met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uLysMetAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATCGCTGGCCTCTACTCAATCGCGTCGACATTTG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     933 TGTTTCTGGCGCGCGCTATTCCGCAATTCATGCCGCAACAGCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 pPheThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1059 CTCAACGGATTGCTCTATGGATTAAAGGACCAAAGCAGATGAAGGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIle......Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 yrGlnArgLeuAlaLysTrpIleAspGly......
                                                                                                                                                                                     Sequence 1200 BP; 285 A; 309 C; 305 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                Length: 219
Gaps: 8
Percent Identity: 21.005
which L-homoserine resistance is enhanced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 TATGACCACCTCGCTCAACCACGGTTATCCGGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                to: 1200
                                                                                                                                                                                                                                                                122.00
1.119
49.772
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US-09-466-935-4 x Z94405
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Ratio:
                                                                                                                                                                                                                                                                                                        Percent Similarity:
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The present sequence is the L-homoserine resistance gene, rhtB, from Escherichia coli. This sequence may be used to impart L-homoserine resistance on E. coll bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tokhmakova IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belareva AV,
                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48442
                                                                                                                                                                                                                           L-homoserine resistance; L-homoserine synthesis; rhtB;
L-threonine; L-valine; L-leucine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1231 BP; 291 A; 319 C; 311 G; 310 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 219
Gaps: 8
Percent Identity: 21.005
                                                                                                                                                                                                E. coli L-homoserine resistance gene, rhtB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 1231
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
557..1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 12-13; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                     "RhtB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: A48442 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98RU-0123511.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-0125406
                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= '
                                                                                                                                                                    (first entry)
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                                                                                                         A48442 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AJIN ) AJINOMOTO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-414602/36.
                                                                                          seg_documentation_block
                                                                                                                                                                                                                                                                           Escherichia coli.
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Quality:
                           1159 GGCGAGG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
204 eSerArg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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                                                                                                                                                                    08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                    EP1013765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                    A48442;
                                                                                                                                                                                                                                                                                                         Key
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10 MetValHisIleValAlaLeuMetSerProGlyProAspPhePheVa 26

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RBS

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Novel gene encoding marine mela from Shewanella - useful as selectable marker in genetic engineering and for inducing larval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colvelliana melA gene (T06766), and was designated m19A (mel-linked gene). The role of the encoded protein (R87577) was unclear as deletion subcloning in E. coli demonstrated that only melA was required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 TIGGIGAGCTAGCAGGCGTTGCCTCGTGGCGATTGCCGCCGTAATGGGT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 CATGACTCTCGGTATGACTATCGGTGTGCGCCGAACCTTATGGATGATGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 GTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAAAATG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 laLeuLysLysGluAlaValSerAlaProAlaProGlnValGluLeuAla 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 AAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATC.....418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 euGlyIleThrCysGlyValMetValTrpAlaGlyIleAlaLeuLeuGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 .......AlaValSerArgSerArgLysGluAlaMetMetGlyValL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 720 BP; 180 A; 165 C; 165 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ProAspPhePheValSerGlnThr..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 203
Gaps: 7
Percent Identity: 25.123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lign seg 1/1 to: T06767 from: 1 to: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                         (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                           93US-0148945.
90US-0496804.
92US-0974837.
                                                                                                                                                                  90US-0496804
154..159
/*tag= a
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Quality: 111.50
Ratio: 0.987
Percent Similarity: 55.665
                                                                                                                                                                                                                                                                                                                                                       Fuqua WC, Weiner RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ignment_block:
IS-09-466-935-4 x T06767
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-039515/04.
P-PSDB; R87527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for melanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oyster settlement
                                                                                                                                                                                                           08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                  21-MAR-1990;
                                                                       US5474933-A
                                                                                                                    12-DEC-1995
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The WelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber and wood.
                                                                                                                                                                                                                               Sequence 720 BP; 180 A; 165 C; 165 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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0.987
55.665
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US-09-466-935-4 x V08533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leullelle 204
                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      697
                                           2222×8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the Shewanella colwelliana MIGA protein, which is related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marine bacterium; melanin synthesis; marine exopolysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MelA melanin protein from marine bacteria - useful as UV blocker e.g. cosmetics % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) +\frac{1}{2}\left( \frac{1}{2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 nProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValGlyA 142
                                                                                                                                                                                                                                                                                                                                                                                               159 GluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGl 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleHis 201
                                                                                                                                                          466 TCCAAAAGGCTGGGCCTTTATGATCTCGCTGCTCCCCCCTTTTATCAGCG
                                                                                                                                                                                                                                                                                                             516 TTGACCAAGCGATTGCACCACAATTAATGGTATTACTGTCAATTATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 .... CGGCGGAAAACCCTTAAACTGTTTTAAGTCGAGGCGATAACATCA
                                                                                                                                                                                                                                    142 spAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:V08533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. colwelliana MlgA coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
167..628
/*tag≈ a
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90US-0496804.
92US-0974837.
93US-0148945.
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ID V08533 standard; DNA; 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuIleIle 204
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21-MAR-1990;
10-NOV-1992;
08-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V08533;
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93 laLeuLysLysGluAlaValSerAlaProAlaProGlnValGluLeuAla 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
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                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                      516 TIGACCAAGCGATTGCACCACAATTAATGGTATTACTGTCAATTATTATG
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                                                                                                                                                                                                                      128 CCGACCITITITICGICICAATIACACCAGGIAIGIGIAIGACACIGGC
                                                                                                                                                                                                                                                                                                                                                                                                                        LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 LysSerGlyArgSerPheLeu...LysGlyLeuLeuThrAsnLeuAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 GluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .... CGGCGGAAAACCCTTAAACTGTTTTAAGTCGAGGCGATAACATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AAGGGAAATGGCCAACCTTGACAATACCTCCAGTCAGATC.....
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                                                                                                                                                                                 21 ProAspPhePhePheValSerGlnThr.........
Length: 203
Gaps: 7
Percent Identity: 25.123
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us-09-466-935-4.rng

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1433 CGGGTTTGGGTAAAGCCCCATGTTGATGGCAATCGTGCTGACTGGTTGAA 1482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1661 rggarcaacgrcgrcgrgcagrrgrgargaccgcarrggccarcaaacr 1710
  072 GICCAICGGACCGCAGAAIGIACIGGIGAIIAAACAAGGAAIIAAGCGC. 1120
                                                                                                                                                                                                                                 .....GAAGGACTCATTGCGGTTCTTCTCGTGTGTTTAATTTCTGAC 1162
                                                                                                                                                                                                                                                                                                                                       1163 GTCTTTTTGTTCATCGCCGCCACCTTGGGCGTTGATCTTTTGTCCAATGC 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1292 GCCATGACAAACAAG......GTGGAAGCGCCACAGATCATTGAAGA 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..... Gregeegeeraracgeegacaccegacgeregarriregeeger 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611 reseccedadearrereacececcecrereasececaagereresec 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....PheLeuLysGlyLeuLeuThrAsnLeuAlaAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 LeuileileValGluThrLeuAlaTrpPheThrValValAlaSerLeuPh 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e......hlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 euPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAla 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euProGlnMetArgArgGlyTyr.....GlnArgLeuAlaLysTrplle 187
                                                                                                                                                                                                                                                                                                                                                                                              .......IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetV 76
                                                                           tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 alGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGly 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1333 AACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCGGGTTCGGCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nProLys......AlaIleIleTyrPheGlySerValPheSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AlaLeuLysLysGluAlaValSerAlaProAlaProGlnVal.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                        51 ValTrpAlaGlyIleAla...LeuLeuGlyLeuHisLeu.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1213 CGCGCCGATCGTGCTCGATATTATGCGCTGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:

ID A52691 standard; DNA; 636 BP
XX A52691;
XX
DT 03-JAN-2001 (first entry)
XX
XX
DE Escherichia coli yggA gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
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                                                                                                                                                                                                                                       1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed addittive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.

NB. This sequence has been created from the information given in table 2
                                                                                                                                                                                                          LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                         DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 other;
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Gaps: 13
Percent Identity: 23.574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1723..2373)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23 and 26; Page -; 16pp; German.
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
complement (82..954)
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                                                                                                                                                                                                                                                                                                                                                                                           /*tåg= a
/label= LysG
1016..1726
T96816 standard; DNA; 2374 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/label= LysE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/label= orf3
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                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                     (first entry)
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0.900
45.627
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US-09-466-935-4 x T96816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-333867/31.
P-PSDB; W37714-16.
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                                                                                                     12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
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of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. coli; yfiK gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
                                                                                                                                                             438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 rValValAlaSerLeuPheAla.....LeuProGlnMetArgArgGly. 179
                                                                                                 254 TIGGCGCTITIAAAACAGCAATGAGCAGTAATATTGAGTTAGCCAGCGCC 303
                                                                                                                                                                                                                                                                            120 uThrAsnLeuAla.........AsnProLysAlaileIleTyrPheG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 TrpGlyIlePheAlaLeu...IleIleValGluThrLeuAlaTrpPheTh 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 TGGTCTGGCTCTTCTCGCTGGCTGGCACCGCGTCTGCGCAA 532
                                                                                                                                                                                                                                                                                                                     104 GCTGGCGCTGGTCACCTGGGGCGGCGTAGCCTTCTTGCTGTGGTATGGTT
                                                     87 yrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                133 lySerValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ..TyrGlnArgLeuAlaLysTrpIleAspGly 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 AAGCACAGCGCATTATCAATCTGGTTGTGGGA 564
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/*tag= a
/product= "Yfik"
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99RU-0104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli yfik gene
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ID A52690 standard; DNA; 588
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P-PSDB; B01788.
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Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1016710-A2
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Troshin PV;
                         E. coli; yggA gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakanishi K, Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 636 BP; 120 A; 143 C; 180 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 194
Gaps: 9
Percent Identity: 27.835
                                                                                                                                                                Location/Qualifiers
1..636
/*tag= a
/product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 24; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0125263
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99RU-0104431
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1.030
51.546
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US-09-466-935-4 x A52691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-414802/36.
P-PSDB; B01789.
                                                                                                                 Escherichia coli.
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Quality:
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                                                                                                                                                                                                                                                                                                                 EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1999;
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31-AUG-1995 (first entry)
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Wen D;
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                            The present sequence is the yflk gene (an excretion protein gene) of Escherichia coil. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 leTyrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 TGTAC..........GGTGTT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 GluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyAr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 gSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 CAGCTTTTGGGCCAGCTTTGCTTTGTGAACGTCAAAATCATTT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GACGCCAGGACCGAACAATATTCTCGCCCTTAGCTCTGCTACGTCGCATG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 GATTTCGTCAAAGTACCCGCGTGCTGGCAGGGATGAGTCTGGGATTTTTG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 AGTGATTGACCCGGCAGCGGTACAC...CTTTTGAGTTGGGCGGGGGGGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CATATATGTCTGGCTGGCGTGGAAATCGCCACCAGCCAACAAGGAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 ...... ValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIl 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 ATTGTGATGTTACTGTGCGGGCATTTCA.....TTTTCACTGGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....AAACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 elleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 euTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:Q80215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGly.....
                                                                                                                                                                                                                                                                                            Sequence 588 BP; 113 A; 134 C; 167 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 22.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 pPheThrValValAlaSerLeuPheAlaLeu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 GGTAGTTGGCGTCAGCGTTTTGCTGGCGATG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 GACGGACTTCAGGCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 CTTTTAAGTGCTTTTTGGACTTACACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
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ID Q80215 standard; DNA; 1063 BP
                                                                                                                                                                                                                                                                                                                                                                                                                    101.00
1.010
56.497
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                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                080215
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factors (NDF's). The perildes encoded by these CDNA clones isolated from human tissues and cell lines, possess the ability to stimulate human pl8-neu tyrosine phosphorylation. These peptides have the ability to induce a differentiated phenotype in certain cell lines and can stimulate or inhibit proliferation of certain cell lines. The NDF's can be used to treat wounds, tumours derived from epithelial tissue of the breast, stomach etc., gastrointestinal disease, Barrett's ossophagus, (non-)oystic kidney disease or inflammatory bowel disease. These cDNA sequences may be used in a recombinant plasmid for the recombinant production of the NDF's in a pro- or eukaryotic host cell.
                                                    Alpha; beta; neu differentiation factor; NDF; human; rat; p185-neu; ytyosine phosphorylation; differentiation; phenotype; proliferation; wound; tumour; epithelial tissue; breast; stomach; gastrointestinal disease; Barrett's oesophagus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences given in Q80215-22 encode human neu differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant neu differentiation factors and corresp. are used in the treatment of tumours, dermal wounds, and gastrointestinal, kidney and inflammatory bowel diseases.
                                                                                                                                                                 (non-)cystic kidney disease; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1063 BP; 291 A; 311 C; 246 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1063
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Percent Identity: 27.919
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                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= Human NDF clone P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 28; Page 125-127; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pierce GF,
                                                                                                                                                                                                                                                                     Location/Qualifiers
12..1055
/*tag= a
Human NDF-alphala clone P2 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.50
1.005
48.731
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US-09-466-935-4 x Q80215/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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Percent Similarity:
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                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporvalatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporvalant; antiparthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiabetic; hypotensive; dermatological; immunosuppressive; antitinfammatory; antibacterial; antivizal; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, cardiovascular disease, disorders may expense and used to treat cancers, proliferative disorders, cardiovascular disease, disorders may expremant to the second processing the proteins in an antiparial and an action and cartilage damage, nocturnal heamoglobinuria, antiminammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 uAlaValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyArgS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 erPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIle 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 TyrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThrTh 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 leValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CGCGCCGGCCTTGCAGATGCTGGTACTGAGCGGCGTGTTCATGGCGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 TyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 PACCIGCIGIACCIGGCCIAIGCCACCIGGCGIGAC.....CGCICGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 401 BP; 57 A; 121 C; 124 G; 98 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 136
Gaps: 6
Percent Identity: 25.735
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31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127736.
05-APR-1999; 99US-017728.
30-MAR-2000; 2000US-0540763.
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1.277
54.412
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                                                                                                                                               (CURA-) CURAGEN CORP.
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US-09-466-935-4 x C74616
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                                                                                                                                                                                                                                                               WPI; 2000-6023
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                                                                                                                                                                                                     Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
      cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipscriatic; antiparkinsonian; nootropic; neuroprotective; antiporvalsant; osteopathic; antiparkintic; immunosuppressant; cardiant immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive, antidiabetic; antidiabetic; antival; antival; antifungal; antifungal; antihemmatic; antiparcoid; antianamic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarchritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodefictency; malaria; autoimmune disorder; asthma; allergy; aplastic anamia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaqulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GGTCATG......CAGCTTTTTCCGCTGTTTGTTTGCAGTAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 TATGGTCAGCACTCTCTTCTGGTACAGCTCCTCCGCCTCCAATAAATTCAA 142
:::||| ::: ||| 457 CTGGTGGAAAGGATGTCTCTGGTTCTCTCTCTCAACAATATGCTCACTGGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ly.Thr......ThralaArgTrpGlyIlePheAlaLeuIl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 elleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euProGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGly 189
                                                                                                                                                                                                                                                                                                                                                                        338 ......CCCATTGGCAATGTTCATCATATTGTTTCG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......AGATGCTTTTCTTGGTTTTGGACT 113
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                                                                                                                                            407 GATGACGTTTTTAGATACGTATTGATTCACCAGCTGGACATTCTCGGGGG
                                                                                                                                                                                                  78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL
                                                                                                                                                                                                                                        308 TICAGACCG......AAGGCICIGCCGAAGAC
                                                                                                                                                                                                                                                                                                                  95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCCACCACACACATGATGCCGACCACAAGGAGGGCGGATGCAGATGCCGGT
                                                                                  63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseg/geneseqn/NA2000.DAT:C74616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 PheAlaGlyAlaLeuPheAlaGlyPheGlyIleHisLeu 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; contraceptive; ss
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ID C74616 standard; cDNA; 401
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This invention decribes novel human nucleic acid sequences from tumor breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer. 233611-248617 represents expressed sequence tags described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human nucleic acid sequences and protein products from tumor breast
tissue, useful for breast cancer therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; EST; human; breast; cancer; gene therapy; treatment; tumour; cytostatic; medicament; ss.
                                                                                                                                        289 ......CGTCGTGCAGTGGTCGCCACGTGGCAGAACTGGCT 329
                                                                                                                                                                                                              187 eAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleHisLeuIleI 204
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                                                                                                                                                                                                                                                     330 GCGACGCAGTTTTGCCGCCCTTTGCCGGGCTGGAGTTGAACCTGGCGT
                                                                                       174 ProGlnMetArgArgGlyTyr.....GlnArgLeuAlaLysTrpIl
245 CGCTTGCAGTGTTTGTGCTGTATGGCCTGTTGGCGAATGTGTTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseg/geneseqn/NA1999.DAT:233622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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ID 233622 standard; cDNA; 1597
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                                                                                                                                                                                                                                                                                                                                            204 leserArg 206
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53 AlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTr 69

from: 1 to: 1597

to: Z33622

Align seg 1/1

alignment\_block: US-09-466-935-4 x Z33622

Length: 180 Gaps: 11 Percent Identity: 27.778

90.50 1.077 46.667

Quality:
Ratio:
Percent Similarity:

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284 GGAATITICATIGGICATIAFGCIGAAAATGITTCIATGGI..ATATT 330
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                                                                                                                                        86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAla... 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 AGCCGCTGGGGGTATTTCTTTTACAGAAT......GCTGG 453
                                                                                               92
                    21
                                                           pleuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetG 86
GCCTAGCAATT.....GGTGCTTTTTACTGAAGGCTTATCAAGTGGT
                                                                                                                                                                                                                                                        137 TTAAGTACTTCTGTTGCTGTTCTGTCATGAGTTGCCTCATGAATTAGG
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TTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGT
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                                                                                                 G.....ATGGTGATAATGGGTGATGGCCTGCACAATTTCAGCGATG
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6.95

us-09-466-935-4.rni

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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-847-743B-23 - 74.00 134.11 6.95
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-456-201-23 - 74.00 134.11 6.95
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-456-241-23 - 74.00 134.11 6.95
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-04295A-23 - 74.00 134.11 6.95
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-922-837-1 73.50 133.59 7.42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
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                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-476-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/476,254
FILING DATE: 06-JUN-1995
CLASSIPECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III. JAMES A.
REGISTRATION NUMBER: 31,714
REGISTRATION NUMBER: JAP30319C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Percent Identity: 25.123
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                                                                                                                                                                                                                             seq_documentation_block:
Sequence 6, Application US/08476254
Fatent No. 5846531
GENERAL INFORMATION:
APPLICANT: WEINER, RONALD M.
APPLICANT: WEINER, RONALD M.
TITLE OF INVENTION: MARINE MELA GEN
WINNER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
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US-09-466-935-4 x US-08-476-254-6
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NO
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 base pairs
nucleic acid
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COMPUTER: IB
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                                                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
      out_format : pfs
OM of: US-09-466-935-4 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query; US-09-466-933-4
Query length: 206
Database: Issued_Patents_NA:*
Database sequences: 302621
Database length: 87301344
Search time (sec): 80.320000
                                                           Date: May 6, 2001 3:40 PM
                                                                                                                                                                                                       Command line parameters:
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|    | 21                                             | ProAspPhePheValSerGlnThr29                                                                                                                     |
|----|------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
|    | 128                                            |                                                                                                                                                |
|    | 30                                             | AlaValSerArgSerArgLysGluAlaMetMetGlyValL 43                                                                                                    |
|    | 178                                            | CATGACTCTCGGTATGAGTATCGGTGTGCCCCGAACCTTATGGATGATGG 227                                                                                         |
|    | 43                                             | euglyllethrCysGlyValMetValTrpAlaGlylleAlaLeuLeuGly 59<br>::    :::        ::          <br>TrGGTGAGCTAGCAGTGCCTTGCCGTGGCGATTGCGCGCGTAATGGGT 277 |
|    | 60                                             | LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa 76 ::: ::::::::::::::::::::::::::::::::                                                     |
|    | 76<br>328                                      | GlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuargGlyA 93<br>                                                                                       |
|    | 93<br>378                                      | laLeuLysLysGludlaValSerAlaProAlaProGlnValGluLeuAla 109                                                                                         |
|    | 110                                            | LysserglyArgserPheleuLysGlyLeuLeuThrAsnLeualaas 125<br>    :::   :::::::::::::::::::::::::::                                                   |
|    | 125                                            | nProLysAlailelleTyrPheGlySerValPheSerLeuPheValGlyA 142<br>        :::::::::::::::::::::::::::::                                                |
|    | 142                                            | spasnvalglyThrThralaArgTrpGlyIlePheAlaLeuIleIleVal 158 ::: :: :: :: :: TTGACCAAGCGATTGCACCACAATTAATGGTATTACTGTCAATTATTATG 565                  |
|    | 159                                            | GlufhrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGl 175                                                                                         |
|    | 175<br>595                                     | nMetArgArgGlyTyrGlnArgLeu                                                                                                                      |
|    | 184                                            | aLysTrplleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleH 201<br>       ::::: ::::       :::   :::<br> CAAGTGGATGACGCATAGCAGGAGTTTAATGATGTGTGTTTGTT   |
|    | 201                                            | isLeullelle 204<br>    :::<br> GGTGGCGCTA 705                                                                                                  |
| S  | ed_name                                        | : /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-847-743B-7                                                                                           |
|    | eq_documer<br>Sequence<br>Patent NC<br>GENERAL | US/07847743B                                                                                                                                   |
|    | TITI TITI NUMB                                 | ENTION: Str<br>ENTION: Her<br>QUENCES: 30<br>CE ADDRESS:                                                                                       |
|    | Z W C W E                                      | ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California                                        |
|    | OO W W                                         | COUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible                         |
| •• | Š                                              | PERATING SISTEM: PC-DUS/MS-DUS                                                                                                                 |

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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: US-07-847-743B-7 from: 1 to: 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1152 GGGTGACAGT...AGTGGAGTGATGGGC.....TGTGGAAGTATAGTGA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1011 G......TGGGTT.....AGGATGGTGAGG...... 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       962 TTCAGACCG................AAGGCTCTGCCGAAGAC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu.....62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 199
Gaps: 12
Percent Identity: 26,131
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24 -May 1991
PRIOR APPLICATION DATA:
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REGISTRATION UNMBER: 27,043
REGISTRATION UNMBER: 27,043
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TELEPHONE: 415/266-1489
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US-09-466-935-4 x US-07-847-743B-7/rev
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Ratio: 0.938
Percent Similarity: 48.241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Single; TOPOLOGY: linear US-07-847-743B-7
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| 145 1y ThrThrAlaArgTrpGiyilePheAlaLeuil 156                                                                |          |
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| euproglimetargrillisi                                                                                      |          |
| 178ArgGlyTyrGlnArgLeualaLysTrpIleAspGlyPhe 190 ::::::: :::                                                 |          |
| seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-096-277-7                                                |          |
| seq_documentation_block: ; Sequence 7, Application US/08096277 ; Patent No. 5578482 . GENERAL TROPARATION. |          |
| n, Marc E<br>Ruth<br>: Ligand Growth Factors that Bind to the                                              |          |
| bb-2 Receptor Protein and Induce Cellular<br>8                                                             | Response |
| ADDRESSEE: Banner, Birch, McKie & Beckeet ; STREET: 1001 G Street, N.W.                                    |          |
| CITY: Washington STATE: D.C. COUNTRY: U.S.                                                                 |          |
| 2IP: 20001<br>; COMPUTER READABLE FORM:                                                                    |          |
| ; MEDIUM TYPE: Floppy disk<br>; COMPUTER: IBM PC compatible                                                |          |
| CPERATING SISIEM: PC-DOS/MS-DOS COFTWARE: PatentIn Release #1.0, Version #1.25 CTEDERN ADDITION THE        |          |
| SOURCE TELEGRICAL US/08/096,277 FILING DATE: 26-JUL-1993                                                   |          |
| ; CLASSIFICATION: 514<br>; PRIOR APPLICATION DATA:                                                         |          |
| ; APPLICATION NUMBER: US 07/875,788<br>; FILING DATE: 29-APR-1992                                          |          |
| ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/640,497 ; FTIING DATE: 14-LAN-1991                   |          |
| PRIOR APPLICATION DATA: APPLICATION NIMBER: 115 07/917,988                                                 |          |
| FILING DATE: 24-JUL-1992                                                                                   |          |
| ; APPLICATION NUMBER: US 07/872,114<br>; FILING DATE: 22-APR-1992                                          |          |
| ; PRIOR APPLICATION DATA:<br>; APPLICATION NUMBER: US 07/528,438                                           |          |
| ; FILING DATE: 25-MAY-1990<br>; ATTORNEY/AGENT INFORMATION:                                                |          |
| ; NAME: Hoscheit, Dale H<br>; REGISTRATION NUMBER: 19,090                                                  |          |
| 85                                                                                                         |          |
| ; TELEPHONE: 202-508-9100<br>; TELEFAX: 202-508-929                                                        |          |
| TELEX: 19/430 BBMB UT ; INFORMATION TO DE NO. 7:                                                           |          |
| 4 X                                                                                                        |          |
| ; STRANDEDNES, both                                                                                        |          |
|                                                                                                            |          |

DNA (genomic)

Align seg 1/1 to reverse of: US-08-456-201-7 from: 1 to: 2199 1111 CIGGIGGAAAAGGAIGICICIGCIICTCICICAAAAAAATAIGCICACIGGA 1062 1061 GATGACGTTTTTAGATACGTATTGATTCACCAGCTGGACATTCTCGGGGG 1012 95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111 20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35 35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52 95 63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl 78 78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu...... Length: 199 Gaps: 12 Percent Identity: 26.131 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
FILING DATE:
APPLICATION NUMBER: U7/080,917
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/70526
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/790801
ATTORNEY AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 712P4
REFERENCE/DOCKET NUMBER: 712P4
TELECHOMB: 415/266-1489 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201 ADDRESSEE: Genentech, Inc. TyreEr: 460 Point San Bruno Blvd CITY: South San Francisco STATE: Callifornia alignment\_block: US-09-466-935-4 x US-08-456-201-7/rev TELEFAX: 415/952-9881 TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single 2199 bases USA Quality:
Ratio:
Percent Similarity: 94080 alignment\_scores: COUNTRY: LENGTH:

us-09-466-935-4.rni

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336 GGTCATG......CAGCTTTTTCCGCTGTTTCTTGGTTTTGCAGTAG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 TATGGTCACACTCTTTTTGTACAGCTCCTCCGCCTCCATAAATTCAA 796
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795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746
992 ......CCCATTGGCAATGTTCATCATATTGTTCG 963
                                                                                                     112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                       962 TTCAGACCG..................AAGGCTCTGCCGAAGAC 937
                                                                                                                                                                                                                                              128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
                                                                                                                                                                                                                                                                                                                                                                                          145 ly.Thr......ThrAlaArgTrpGlyIlePheAlaLeuIl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 GCCACCACACACATGATGCCGACCACAAGGAGGGCGATGCAGATGCCGGT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 elleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 euProGlnMetArg......177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-456-241-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGGTTT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REAABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE CORRENT APPLICATION NOTION DATA: APPLICATION NOTION DATA: APPLICATION NOTION: 31-MAY-1995 CLASSIFICATION DATA: APPLICATION NOTION: 08/126145 FILING DATE: 23-SEP-1993 FILING DATE: 23-SEP-1993 FILING DATE: 11-MAY-1992 PRIOR APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: APPLICATION NOTION: 07/9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
CUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
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to: 2199 1152 GGGTGACAGT...AGTGGAGTGATGGGC.....TGTGGAAGTATAGTGA 1112 1111 CTGGTGGAAAGGATGTCTCTGCTTCTCTCAACAATATGCTCACTGGA 1062 111 112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128 128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145 .....ThralaArgTrpGlyIlePheAlaLeuIl 156 156 elleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173 ::::|||:::||||||| |||::::||
845 TATGGTCAGCACTCTCTTCTGGTACAGCTCCTCCGCCTCCATAAATTCAA 796 795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746 962 TTCAGACCG..............AAGGCTCTGCCGAAGAC 937 173 euProGlnMetArg......177 95 20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35 35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52 78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 1011 G.....TGGGTT....AGGATGGTGAGG..... 95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu....... 63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl .....ArgGlyTyrGlnArgLeuAlaLysTrplleAspGlyPhe 190 745 CCAGIAAACICATTIGGGCACTIGCACAAGIATCICGAGGGTIT 701 Length: 199 Gaps: 12 Percent Identity: 26.131 Align seg 1/1 to reverse of: US-08-456-241-7 from: 1 00,000 712P4C1D1 alignment\_block: US-09-466-935-4 x US-08-456-241-7/rev NAME: Lee, Wendy M.
REGISTRATION UNUBER: 712P4
REFERENCE/DOCKET NUMBER: 712P4
TELECOMMUNICATION INFORMATION:
TELEFAN: 415/252-1994
TELEFAX: 415/252-1994
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 bases
TYPE: nucleic acid
STANDEDNESS: single 0.938 90.06 145 ly.Thr..... Quality:
Ratio:
Percent Similarity: alignment\_scores: US-08-456-241-7 178

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20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35
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seq_documentation_block:
; Sequence 7, Application US/08550815
; Patent No. 5869618
; GENERAL INFORMATION:
; APPLICANT: Lippman, Marc E
APPLICANT: Lippman, Marc E
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Gaps: 12
Percent Identity: 26.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,815
FILING DATE: 31-OCT-1995
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/096,277
FILING DATE: 26-5UL-1993
APPLICATION NUMBER: US 07/875,788
FILING DATE: 29-6PR-1992
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/640,497
FILING DATE: 14-70R-1991
PRIOR APPLICATION NUMBER: US 07/917,988
FILING DATE: 24-3UL-1992
PRIOR APPLICATION NUMBER: US 07/917,988
FILING DATE: 24-3UL-1992
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/872,114
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REJISTRATION NUMBER: 19,090
REFERENCE-POCKET NUMBER: 02)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-508-9299
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0.938
48.241
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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CLASSIFICATION:
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-550-815-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || || || || 895 GCCACACACATGATGCCGACCACAAGGAGGGGGGGATGCAGATGCCGGT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::::|||:::|||||||| |||:::::
845 TATGGTCAGCACTCTCTCGGCTCCAGCACACAAAATTCAA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 euProGlnMetArg......177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746
                                                                                                                                                                                                                                                                                                             1011 G.......rgggrr.....aggarggrgAgG..... 993
                                                                                                                                                                                                                                                                                                                                                         95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 eIleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                        52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu....... 62
                                                                                                                                                                                                                                                                   78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 95
35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT
                                                                                                                                                                                                                                                                                                                                                                                            ........CCCATTGGCAATGTTCATCATATTGTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl
                                                                                                                                                                              63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-703-089-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGTTT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banner, Birch, McKie & Beckeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/703,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1001 G Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-04295A-7
                                                                             .....ThrAlaArgTrpGlyIlePheAlaLeuIl 156
                                                                                                                                                                                            895 GCCACCACACACATGATGCCGACCAAAGGAGGGCGATGCAGATGCCGGT 845
                                                                                                                                                                                                                                                                                845 TATGGTCAGCACTCTCTCTGGTACAGCTCCTCCGCCTCCATAAATTCAA 796
                                                                                                                                                                                                                                                                                                                                                  173 euProGlnMetArg......177
156 eIleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                    795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746
                                               seq_documentation_block:
    sequence 7, Application PC/TUS9204295A
    GENERAL INFORMINGN:
    TILE OF INVENTION: Structure, Production and Use of TILE OF INVENTION: Herequlin
    NUMBER OF SEQUENCES: 30
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGGTTT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04295A
FILING DATE: 19920521
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: 07/705212
APPLICATION NUMBER: 07/705212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 06-NOV-1991
PRIOR APPLICATION DATA: 7743
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hensley Max D. REGISTRAION NOMBER: 27,043 REFERENCE/DOCKET NUMBER: 711 TELECHONE: 415/225-1994 TELEFNX: 415/295-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: linear
962 ITCAGACCG...
                                                                                                                                                   145 ly.Thr.....
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us-09-466-935-4.rni

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Align seg 1/1 to reverse of: US-08-390-878-17 from: 1 to: 15239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4922 .......CCGCGTGCGCTCAATGTCGTCAAGTTTGGCGGCGCGCCCT 4883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14782 GACCTGTGCGGCATTCACGTTCCTC......A 4757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 rProGlyProAspPhePhePheValSerGlnThrAlaValSerArgSerA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 rgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetVal 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 yrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGlu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LeumetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSe 18
STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 TrpAlaGlyIle......AlaLeuLeuGlyLeuHisLeuIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 eGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 Ala... ValSerAlaProAlaProGlnValGluLeuAlaLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 11
Percent Identity: 22.120
                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/390,878 FILING DATE: 17-FEB-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              CLASSIPICATION: 435

TOTORNEY AGENT INFORMATION:
NAME: HUNCEY. TOM
REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 15371A-17

TELECOMUNICATION INFORMATION:
TELECHAX: 415/543/9600

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5090 CTGGCCTGCTTCACGCTGATCGCCGCGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-466-935-4 x US-08-390-878-17/rev
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.00
                      STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
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Quality:
                                                                                                             94105
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Page 9

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seq_documentation_block:

Sequence 3, Application US/08311023

Patent No. 5693465

Better No. 5693465

APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, ROBERT III APPLICANT: MICHOLSON, ROBERT III OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: BREAST TUMOURS
NUMBER OF SEQUENCES:
ADDRESSEE: YOUNG & Thompson
STATE: VA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1177 AGCCGCTGGGGGTATTTCTTTTACAGAAT......GCTGG 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                        106 ......ValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 euThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPhe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 SerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePh 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 eAlaLeuIleIleValGluThrLeuAlaTrpPheThrValValAlaSerL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 ... ArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGl 192
                                                                                                                                                                                                                                                                       787 GCCGGCGTCGCCACTTTG.....GCCTG 809
                                                                                                                                                                                                                                                                                                                                                                   810 G......ATGGTGATAATGGGTGATGGCCTGCACAATTTCAGCGATG 850
                                                                                                                                                                                                                                                                                                                                                                                                               86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAla... 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 895 TTAAGTACTTCTGTTGCTGTTTCTGTCATGAGTTGCCTCATGAATTAGG 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        945 TGACTTTGCTGTTCTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCC 994
                                                                                                                                                                                                                         53 AlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTr 69
                                                                                                                                                                                                                                                                                                                     69 pLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 179
Gaps: 11
Percent Identity: 27.374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euPheAlaLeuProGlnMet..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 yAlaLeuPheAlaGlyPheGlyIleHisLeuIleIle 204
                                                                                                                                                                                from: 1
                                                                                                                                                                              Align seg 1/1 to: US-08-311-023-1
                                                                                                              alignment_block:
US-09-466-935-4 x US-08-311-023-1
                    86.50
1.042
46.369
                                              Ratio:
Percent Similarity:
                       Quality:
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
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us-09-466-935-4.rni

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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM:
COMPUTER: Detentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY AGENT INFORMATION:
RESISTRATION NUMBER: Reg. No. 5693465 32,925
RESISTRATION NUMBER: WCM.56
TELEPHONE: 703/685-0573
TELEPHONE: 703/685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1111111 ::: ||| | | | ||| || ::
1089 TGCACTT......ACTGCTGGCTTATTCATGTATGTTGTTGT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePh 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 eAlaLeuIleIleValGluThrLeuAlaTrpPheThrValValAlaSerL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                810 G.....ATGGTGATAATGGGTGATGCCTGCACAATTTCAGCGATG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAla... 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945 IGACTITICATIONAGECTGCATGACCTAAAGCTGTCC 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 euThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPhe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euPheAlaLeuProGlnMet......176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        895 TTAAGTACTTCTGTTGCTGTTTCTGTCATGAGTTGCCTCATGAATTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 179
Gaps: 11
Percent Identity: 27.374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-311-023-3
                                                                                                                                                                                                                                                                    alignment_block:
US-09-466-935-4 x US-08-311-023-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.50
1.042
46.369
                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-311-023-3
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137
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177 ... ArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGl 192
                                                                                                                                                                    3 MetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerPr 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 oGlyProAspPhePhePheValSerGlnThrAlaValSerArgSerArgL 36
                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-395-246C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 8
Percent Identity: 23.699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-395-246C-1 from: 1 to: 3924
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,246C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35.84
REFERENCE/DOCKET NUMBER: x96!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-27-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-09-466-935-4 x US-08-395-246C-1
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TYPE: nucleic acid
STRANDEDNESS: single
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Ratio: 1.082
Percent Similarity: 45.665
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..3924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                              STATE: II
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us-09-466-935-4.rni

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seq_documentation_block:
Sequence 1, Application US/09335409
Fatent No. 6121029
SGRERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Genes For THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERROCE: 4-30582A
CURRENT FILING DATE: 1999-06-17
UNDBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH 68750
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                                     2497 CAGGAAAACACGACAGGGGGATTAACAGCCACTCTGAGCGGGGGGGACCAA 2546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2738 AGAAAGCATATCAAGAATCAGCTAGTTCTGCTTGTGAGGCAGCCTCTGCC 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 oGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuT 121
                                                                                                                                                                                                                                 54 ly......IleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMet
                                                                                                                                                                                                                                                                                                                                         2638 GGCTGGAAGTTGGCACTGGTGTGCATCTCCGGGTTCCAGCCCTGAT
                                                                                                                                                      39 ....MetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaG
                                                                                                                                                                                                                                                                                                          68 AlarrpLeuHisThrLeuIleMetValGlyGly.....GlyLeuTyrLe
                                                                                                                                                                                                                                                                                                                                                                                            82 uCys.....TrpMetGlyTyrGlnMetLeuArgGlyAlaL
                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-335-409-1
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Gaps: 9
Percent Identity: 22.010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 68750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
36 ysGluAla......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-335-409-1
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US-09-466-935-4 x US-09-335-409-1
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; ORGANISM: Sorangium cellulosum
US-09-335-409-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2820 GGAGGCTTTGCAATCCT 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2788 ATCCGTA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 hrAsnLeuAlaAsnPro 126
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0.845
46.411
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Ratio:
Percent Similarity:
                                                                           38 .....
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1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17

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seq_documentation_block:
Sequence	10, Application US/08940424A
Sequence	10, Application US/08940424A
Sequence	10, Application US/08940424A
GENERAL INFORMATION:	
APPLICANT: Blancr, William S.	
APPLICANT: Gamble, Mary V.	
APPLICANT: Mertz, James R.	
TITLE OF INVENTION: POTENT INHIBITORS OF HUMAN 9-cis RETINOL DEHYDROGENASE	
TITLE TEREBENCE: 0555/544	
CURRENT APPLICATION WUMBER: US/08/940,424A	
CURRENT PILING DATE: 1997-09-29	
NUMBER OF SEQ ID NOS: 13	
SOFTWARE: Patentin Ver. 2.0	
SEQ ID NO 1000	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3881 AGCGCGAGTCGATGCGCCGCAGTATGCGCAGGTGACGCTCGCGGGGG 3930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .........GGCCTCTTCCTCGG 3830
.....GCCTCCGGCGAGCTCGCGCGGCGGC 3511
                                                                                                                                                                                                                                         3652 .......ATAGGCGCGCTCCTCCTGCTGATGGCGGGCATCGAG 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3562 cccrccerc...ercédcececrcececceéerrccarceagecerer 3608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 PheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 ullelleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 MetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAlaProGl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 nValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuThrA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hrLeulleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGln 88
                                                                                    17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-940-424-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3609 CCAGGAGCCGGCGGTCGGGGTCGTGCTCTCGGGCATCTCCTGG......
                                                                                                                                                                                                  34 erArgLysGluAlaMetMetGlyValLeu.....GlyIleThrCysGly
                                                                                                                                                                                                                                                                                                                 49 ValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                   3691 GTCGACGTGGGCATCCTGCGCAAGGAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3931 GTGGTCAGCGAGGTCGCTGCCTGGGTG 3957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 laLeuProGlnMetArgArgGlyTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 .....GlnArgLeuAlaLysTrpIle 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3790 credrecrearescentrecase.
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; ORGANISM: mouse
US-08-940-424-10
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136 heSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp..... 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 ......lleValGluThrLeuAlaTrpPheThr......165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 GAGTACTGAGTGTGAACACACTGGGGCCCATCGGTGTCACCCTTGCCCTG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                             {
    :::||| ||| || ||
263 CTGTGACTTTGGGCGCCTTCTGGCACTGCAACTTGACCAGAAGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLe 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 TCTGGAGCAGAAGACCTGCAGGAGGCCTCCTCCCCGCCTCCACAAC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 uLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValP 136
                                                                                                                                                                                28 nThralaValSerArgSerArgLysGlualaMetMetGlyValLeuGlyI 45
                                                                                                                                                                                                                                                                                      45 leThrCysGlyValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHis 61
                                                                                                                                                                                                                                                                                                                                                                                                                     78 y......GlyLeuTyrLeuCysTrpMetG 86
                                                                                                                                                              12 HislleValAlaLeuMetSerProGlyProAspPhePheValSerGl 28
                                                                                                                                                                                                                                                                                                                                                       62 LeuileileGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 209
Gaps: 9
Percent Identity: 22.488
                                                                                                                           Align seg 1/1 to: US-08-940-424-10 from: 1 to: 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-466-935-4 x US-08-940-424-10
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   Quality:
   Ratio:
   Percent Similarity:
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 6, 2001, 14:40:01; Search time 26.05 Seconds (without alignments)

543.452 Million cell updates/sec

Title:

US-09-466-935-4

Sequence:

1 MLMLFLTVAMVHIVALMSPG......IDGFAGALFAGFGIHLISR 206

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR\_67:\*
1: pir:\*
2: pir::\*
3: pir::\*
4: pir:\*
4: pir:\*\*

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | hypothetical 13.3 | hypothetical prote | Ω      | hypothetical prote |        |        |        | ú      | hypothetical prote |        |        | Ω,     | hypothetical prote | hypothetical prote | conserved hypothet | hypothetical prote | dihydrodipicolinat | dihydrodipicolinat | conserved hypothet | conserved hypothet | conserved hypothet | amino acid transpo | chemotaxis protein | hypothetical prote | Ω      |        |       | hypothetical prote | conserved hypothet |
|-----------|----------------|-------------------|--------------------|--------|--------------------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|-------|--------------------|--------------------|
| SUMMARIES | OI.            | н65186            | F64115             | F82353 | D84016             | B83279 | T43921 | F83444 | H64759 | F83306             | G83082 | C82979 | F83051 | E83703             | C55580             | B82410             | F64940             | G84086             | F69975             | C75329             | G82200             | E82388             | C82523             | T30317             | 876178             | C82471 | G82358 | 213   | D83187             | B69066             |
|           | Length DB      | 1                 |                    | 222 2  |                    |        |        |        |        |                    |        | 206 2  |        |                    |                    |                    |                    | 208 2              |                    | 241 2              |                    | 209 2              |                    |                    |                    |        |        |       |                    | 208 1              |
| æ         | Query<br>Match | 58.6              | 35.0               |        | 27.7               | 26.0   | 25.6   | 25.0   | 24.8   | 23.4               | 23.2   | 19.8   | 19.6   | 19.1               |                    | 18.7               | 18.0               | 17.6               |                    | 16.6               | 16.3               | 15.9               | 15.5               | 15.1               |                    |        | 13.5   | 13.4  | 12.9               | 11.7               |
|           | Score          | 618               | 368.5              | 313.5  | 292                | 274.5  | 269.5  | 263.5  | 261.5  | 246.5              | 245    | 208.5  | 207    | 201                | 199                | 197.5              | 190                | 186                | 180.5              | 174.5              | 172                | 167.5              | 163                | 159                | 15                 |        | 142.5  | 141.5 | m                  | 123.5              |
|           | Result<br>No.  | 1                 | 7                  | 3      | 4                  | 5      | 9      | 7      | 82     | 6                  | 10     | 11     | 12     | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25     | 56     | 27    | 28                 | 59                 |

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Gaps

.; 0 205 SR 206 || |121 SR 122

20 OY OY

Query Match 58.6%; Score 618; DB 2; Length 122; Best Local Similarity 100.0%; Pred. No. 2.6e-48; Matches 122; Conservative 0; Mismatches 0; Indels

| hypothetical prote conserved hypothet hypothetical 15.4 conserved hypothet hypothetical 28K p YggA protein homol hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable amino aci NADH dehydrogenase LyseXYgBA family p iron (III)-transpo hypothetical prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ALIGNMENTS | HESULT 1 He5186 NyAlternate names: hypothetical protein o128 NyAlternate names: hypothetical protein o128 NyAlternate names: hypothetical protein o128 NyAlternate names: hypothetical protein o128 C. Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C. Accession: H55186; S30713 NyAlternate names: hypothetical protein 17-Sep-1997 #text_change 08-Oct-1999 C. Accession: H55186; S30713 NyAlternate number: R64720; MUD: 97426617 A. Title: The complete genome sequence of Escherichia coli K-12. A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65186 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. Accession: H65180 A. 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| B833280<br>B833280<br>D723187<br>D723187<br>QQEC5A<br>QQEC5A<br>C36393<br>C363136<br>C363136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136<br>C683136                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ALIG       | in rec0 3' re al protein ol revision 17 G.; 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Species: Excherichia coli c. Species: Excherichia coli c. Species: Excherichia coli c. C. Date: 12.5ep-1997 * sequence_revision 17-56 C. Accession: H65186; 530713  C. Accession: H65186; 530713  A. Aritle: The complete genome sequence of Excherce 277, 1453-1462, 1997  A. Arcession: H65186  A. Accession: H65186  A. Accession: H65186  A. Molecule type: DNA  A. Cartus: preliminary; nucleic acid sequence A. Molecule type: DNA  A. Experimental source: strain K-12, substrain Manaiells. D. L.; Plunkett III, G.; Burland, Schence 257, 771-778, 1992  A. Ritle: Analysis of the Excherichia coli genome 257, 771-778, 1992  A. Reference number: S30660; MUID:92358234  A. Reference number: S30660; MUID:92358234  A. Status: Preliminary; nucleic acid sequence A. Molecule type: DNA  A. Residues: VANSLLD, 2, LDDATWCTE', 12, RGGE  A. Residues: WANSLLD, 2, LDDATWCTE', 12, RGGE  A. Residues: WANSLLD, 2, LDDATWCTE', 12, RGGE  A. Residues: WANSLLD, 2, LDDATWCTE', 12, RGGE  A. Note: this sequence has been corrected  A. Note: the nucleotide sequence was submitte                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 0 H B B B B B B B B B B B B B B B B B B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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RESULT 4

BA9016

Bydolf

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Bydolf

Lybercleal protein BH2932 (imported) - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Species: Bacillus halodurans

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C;Species: Bacillus halodurans

C;Accession: D84016

R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; H

Nucles. Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

R;Reference number: A83650; MUID:20263314

A;Accession: D84016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-210 <STC>
A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06651.1; GSPDB:G

C;Genetics:

A;Gene: BH2932

C;Superfamily: hypothetical protein b1798
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A)Reference number: BB3279
A)Status: preliminary
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A.; Larbig,
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                                                                          64 YLVKQQDPMLFNLLQLAGGSYLLXLGAGALQSVWAQKNASTPTHSPAPSI-LGNRRQAFTK 122
                                                                                                                                                                                                                                                                                   GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVS----APAPQVELAKSGRSFLK 117
                                                                                                                                                                                                              GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRCA--LKKEAVSAPAPQVELAKSGRS----FLK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEANMGVLGITCGVMVWAGIALLGLHLI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGYQRLAKWIDGFAGALFAGFGIHLII 204
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| RFYQTHSYWFDRFLGAALLFFAIRIII 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 QRMQRITRSVDSICAAVF 200
                                                                                                                                                                                                                                                                                                                                                                                                                             RGYORLAKWIDGFAGALF 195
                      62
                                                                                                                                                                                                                          118
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hypothetical protein H11307 - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Accession: F64115
R; Fleischmann, R.D; Adams, M.D; White, O.; Clayton, R.A; Kirkness, E.F.; Kerlavage, P. R; Fleischmann, R.D; Adams, N.D; White, O.; Clayton, R.A; Kirkness, E.F.; Kerlavage, P. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman, J. Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Recence number: A6400; MUID:95350630
A; Accession: F64115
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-210 < TICR>
A; Residues: 1-210 < TICR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 368.5; DB 2
Pred. No. 8.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon: GTG
C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 RGYQRLAKWIDGFAGALFAGFGIHLI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.0%;
38.8%;
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F8344 X Q; Erwin, A.L; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, R.R.; Kas, A.; Larbig, K.; L.; Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337 A;Reference number: A82950; MUID:20437337 A;Reference number: A82950; MUID:20437337 A;References: GB:AE004589; GB:AE004091; NID:g9947574; PIDN:AAG05009.1; GSPDB:GN A;Experimental source: strain PA01
A;Cross-references: GB:AE004589; GB:AE004091; NID:g9947574; PIDN:AAG05009.1; GSPDB:GN A;Experimental source: strain PA01
C;Genetics: Caperefical protein b1798
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: H64759
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Man, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Reference number: BNA
A;Residues: 1-223 <BLAT>
A;Residues: 1-223 <BLAT>
A;Residues: 1-223 <BLAT>
A;Cross-references: GB;RE000140; GB:U00096; NID:91786520; PIDN:AAC73431.1; PID:917865
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKK------EAVSAPAPQVELAKSGR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LELIYAANVHIYALMSPGPDFFFVSQTAVSRSRKEANMGVLGITCGVNVWAGIALLGLHLI 63 ::||| : : :|| : | : :| | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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C;Superfamily: hypothetical protein b1798
C;Keywords: transmembrane protein
F;26-42/Domain: transmembrane #status predicted <TML>
F;85-101/Domain: transmembrane #status predicted <TM2>
F;163-179/Domain: transmembrane #status predicted <TM3>
F;163-179/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 25.0%; Score 263.5; DB 2;
Local Similarity 27.3%; Pred. No. 1.9e-16;
Les 59; Conservative 46; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: | |: | |: | PALQARLIEALVRA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 POMRRGYQRLAKWIDGFAGALF ---- AGFGIHLIIS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S.
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
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C;Species: Versinia enterocolitica
C;Species: Versinia enterocolitica
C;Species: Versinia enterocolitica
C;Species: Versinia enterocolitica
C;Accession: T43921
S;Saken, E.M.; Rakin, A.V.; Reesemann, J.
S;Saken, E.M.; Rakin, A.V.; Reesemann, J.
S;Damitted to the EMBL Data Library, November 1999
A;Description: Molecular characterization of a novel siderophore-independent iron transp
A;Reference number: Z22724
A;Reference number: Z22724
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: L-121 c,SAR.
A;Residues: L-121 c,SAR.
A;Residues: L-121 c,SAR.
A;Residues: L-121 c,SAR.
A;Residues: L-121 c,SAR.
A;Resimental source: strain WA-314
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F88444
hypothetical protein PA1620 [imported] - Pseudomonas aeruginosa (strain PAOI)
C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VLVRESLALFTALKLAGAAYLVFLGLRML--LAREDSVAEEAAGGAGVSSWAMLRSGFLT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQ 181
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                                                                                                                                                                                                                                                                                                                                                      2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                         Length 204;
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                10 26.0%; Score 274.5; DB 11 22.3%; Pred. No. 1.9e-17 Conservative 42; Mismatches 8
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A;Gene: yfub
C;Superfamily: hypothetical protein b1798
C;Keywords: iron transport
                                                   A,Gene: PA2929
C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 RLAKWIDGFAGALFAGFGIHL 202
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 65; Conserv
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Cycary Colored protein PA5341 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Accession: C82379
R;Strover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nadman, S.; Yuan, Y. S.; Olson, M.V.
A;Reference number: A82950; MUID:20437337
A;Reference number: A82950; MUID:20437337
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A;Reference number: A82950; MUID:20437337
A;Reference number: A82950; MUID:20437
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-210 - GST-0>
A; Residues: 1-210 - GST-0>
A; Cross-references: GST-AE004864; GB: AE004091; NID: 99950740; PIDN: AAG07895.1; GSPDB: GN
A; Experimental source: strain PAO1
A; Experimental source: strain PAO1
A; Genetics:
A; Genetics:
C; Superfamily: hypothetical protein b1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASL---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 RGLLTNLLNPKALLFCSVLLPQFVSPEAGSLA-----VQFAALGTVLVLVGLAFDC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLIIEKMA------WLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSG--RSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTAR-----WGI---FALIIVE 159
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGI----TCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL 60
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                                                                                                                                                                                                                                                                                                            Length 210;
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                                                                                                                                                                                                                                                                                                            Ouery Match 23.2%; Score 245; DB 2; L Best Local Similarity 33.3%; Pred. No. 8.4e-15; Matches 75; Conservative 34; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

19.8%; Score 208.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 1.5e-11;
Matches 65; Conservative 32; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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D
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C:Species: Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83306
R:Stover, C.K.: Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 595-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337
A;Reference number: A82950; MUID:20437337
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: L204 &STO>
A;Cross-references: GB:AE004699; GB:AE004091; NID:99948782; PIDN:AAG06098.1; GSPDB:GNO1
A;Experimental source: strain PA01
C;Genetics: PA2710
C;Superfamily: hypothetical protein b1798
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Discouration of Sa3082
C;Accession: G83082
R;Stover, C.K., Pahan, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Mature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Recession: G83082
A;Status: preliminary
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                                                                                                                118 GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                    64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRS-----FLK 117
    VYLTVGL-FVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATL 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 POMRRGYORLAKWIDGFAGALFAGFGIHLIIS 205
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Best Local Simmatches 62;
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Conserved hypothetical protein VCA0846 [imported] - Vibrio cholerae (group O1 strain C) Species: Vibrio cholerae
C) Species: Vibrio cholerae
C) Species: Vibrio cholerae
C) Species: Vibrio cholerae
C) Species: Vibrio cholerae
C) Species: Vibrio cholerae
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                                        65 EKMAWLHTLIMVGGGLYLCWMGYQMLRGALKK----EAVSAPAPQVELAKSGRSFLKGLL 120
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62 LIIEKMAWLHTLIMVGGG---LYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 216;
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                                                                                                                                                                                                                                                                                                   175 QLLMRSSFIKNQMHR------IKGGLLALIGLQVAFSK 206
                                                                                                                                                                                                                                                   166 -- VVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.9%; Score 199; DB 2; L
illarity 28.4%; Pred. No. 1.1e-10;
Conservative 31; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 ------RRRQRLAAGATSGVGALFVGFGVKL 210
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Best Local Similarity
Matches 62; Conserv
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                                                                         Conserved hypothetical protein PA4757 [imported] - Pseudomonas aeruginosa (strain PA01) Conserved hypothetical protein PA4757 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Dseudomonas aeruginosa C;Date: 15:Sep-2000 #sequence_revision 15:Sep-2000 #text_change 31-Dec-2000 C;Accession: F83051 R;Stover. C.K.: Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Ristover. C.K.: Tory, S. Olson, M.V. Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V. Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Mittle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathola; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathola; A;Stetus: Preliminary A;Moleoule type: DNA A;Residues: 1-216 csTO> A;Cross-references: GB:AE004889; GB:AE004091; NID:g9951014; PIDN:AAG08143.1; GSPDB:GN001 A;Experimental source: strain PA01 A;Cone: PA4757 C;Superfamily: hypothetical protein b1798
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C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Species: Oliver-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C.Species: Darami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
R.Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A.Fitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A.Rocession: E83703
A.Stects: preliminary
A.Speciment type: DNA
A.Stects: Techninary
A.Rocession: E3703
A.Stects: Techninary
A.Stectimental source: strain C-125
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 KAEPMLFIGLKYLGAAYLFYLGVGMLRGAWRKLRNPEATAAQAEQVDV---HQPFRKALL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETL-------AWF 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 216;
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STRAIN=K12 / MG1655;
MEDLINE=$2358234; PubMed=1379743;
MEDLINE=$2358234; PubMett G. III, Burland V.D., Blattner F.R.;
Daniels D.L., Plunkett G. III, Burland v.D., Blattner F.R.;
Fanalysis of the Bscherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
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MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed 5.111, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. 111, Bloch C.A., Perna N.T., Burland V.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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Science 277:1453-1474(1997).
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STRAINE-K12;
MEDLINE-87115164; PubMed-3027506;
Irino N., Nakayama K., Nakayama H.;
The reco gene of Escherichia coli K12: primary structure and evidence for SoS regulation.";
MOI. Gen. Genet. 205:298-304(1986).
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
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NU4M_HALGR
NU6M_CYPCA
NU4M_BRAFL
PTPW_ECOLI
NU6M_CARAU
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COX1_KLULA
COX3_METSE
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Unpublished observations (DEC-1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
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SEQUENCE FROM N.A.
STRAIR*LIZ / Malbes;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
Science 269:496-512(1995).
Science 269:496-512(1995).
-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P75693; P71307;
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 24.8 KDA PROTEIN IN BETT-PRPR INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels
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254D159014845473 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%; Score 368.5; DB 1
38.8%; Pred. No. 8.8e-23;
7ative 42; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA.
                                                                                                                                                                                                                                                                                                                                                                EMBL: 032810; A.
TIGR: HI1307; -
InterPro: IPR001123; -
Fram: FF01810; LysE; 1.
Hypothetical protein; Transmembrane.
T TRANSMEM 42 62 86 POTENTIAL
FT TRANSMEM 126 146 POTENTIAL
TRANSMEM 126 146 POTENTIAL
TRANSMEM 127 167 POTENTIAL
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TRANSMEM 147 167 POTENTIAL
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Best Local S
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 47 AND 73.
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SEQUENCE FROM N.A.

STATAIN-RD / KW20. VARCC 51907;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Relavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shriby R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Otterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1054; DB 1; Length 206; Similarity 100.0%; Pred. No. 2.9e-77; 16; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
Bacteria: proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
VOR_TaxID=727;
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F64017878CC6D50D CRC64;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-ULL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN HI307.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                            EMBL; M87049; AAA67619.1; ALT_FRAME.
EMBL; AE000458; AAC76826.1; ALT_FRAME.
EMBL; M30198; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ORLAKWIDGFAGALFAGFGIHLIISR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QRLAKWIDGFAGALFAGFGIHLIISR 206
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PIR; S30713; S30713.
Eccdene; EG11468; rhtc.
InterPro; IPR001123; -.
Pfan: FF018105; Lyse. I
Transport; Transmembrane.
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67
150
206 AA;
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Matches 206;
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                                      C STRAIN=PAO1;

XN MEDLINE=204333; PubMed=10984043;

XI STRAIN=PAO1;

XI STRAIN=PAO1;

XI STRAIN=PAO1;

XI STRAIN=PAO1;

XI STRAIN=204333; PubMed=10984043;

XI STRAIN=204333; PubMed=10984043;

XI STRAIN=204333; PubMed=10984043;

XI STRAIN=10 E., Mest D.J., Lagrou M.,

XI STRAIN=10 E., Mest D.J., Langrou M.,

XN STRAIN=10 E., Mest D.J., Lin R.M.,

XN STRAIN=10 S. Y. Saler M. H., Mong G.K.-S., Wu Z., Paulsen I.T.,

XN Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XN Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XN Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XN Spencer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

XN Complete genome sequence of Pseudomonas aeruginosa PAO1, an

XN Opportunistic pathogen ";

YN Opportunistic pathogen";

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YN YN STRAIN ACOLIDAN LOCATION: THE CALL ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN ACOLUMN A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 FLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLII 64
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Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
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P76349; 007991; 007959; 007916; 007959; 15-7UL-1998 (Rel. 36, Last sequence update)
15-7UL-1998 (Rel. 36, Last sequence update)
15-7UL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 23.2 KDA PROTEIN IN GAPA-IND INTERGENIC REGION.
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POTENTIAL.
POTENTIAL.
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A -> G (IN REF. 1).
K -> Q (IN REF. 1).
W. A30A08E714591B8D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 TVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHL 202
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EmBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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79 ITQCEEIFSLIRIVGGAYLLWFAWCSMR------RQSTPQMSTLQOPISAPWYVFFRR 130
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (Nov-196) to the EMBL/GenBank/YDBJ databases.
-! SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-! SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 15;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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STRAIN-ATCC 15692 / PAOJ;
MEDLINE-9422830; PubMed-8169201;
KWON D.-H., Lu C.-D., Walthall D.A., Brown T.M., Houghton J.E.
Abdelal A.T.;
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LRLIYEGVTOR -> YA (IN REF. 2).
E17F5ABC31EE3F26 CRC64;
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llarity 28.2%; Pred. No. 3e-14;
Conservative 50; Mismatches 83;
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NETALES 4

YER7_PERE 5TANDARD; PRT; 216 AA.

DY 10-CT-1994 (Rel. 30, Created)

DT 01-CCT-2000 (Rel. 40, Last sequence update)

DT 01-CCT-2000 (Rel. 40, Last sequence update)

DT 01-CCT-2000 (Rel. 40, Last sequence update)

DF 10-CCT-2000 (Rel. 40, Last sequence)

DF 10-C
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X MEDLINE-97251358; PubMed-9097040;

X MEDLINE-97251358; PubMed-9097040;

X Hobine T., Aiba H., Baba T., Fujiak K., Hayashi K., Inada T., Isono K., A. Aiba H., Rimara S., Kitakawa M., Kitagawa M., Makino K., Miki T., A. Michino Y., Morimura K., Marino K., Miki T., A. Mishinoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Savaundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Y., Horluchi T., Saito N., Sampei G., Seki Y., Y., Horluchi T., Saito N., Takemoto K., Wada C., Y., Horluchi T., Saito N., Takemoto K., Wada C., Y., Horluchi T., Saito N., Sammoto Y., Horluchi T., Saito N., Sammoto Y., Horluchi T., Saito N., Saito N., Saito N., Saito N., Horluchi T., Saito N., Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 IVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG-----VMVWAGIALLGLHLIIEKM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 IFIVLVPGPNTLFVLKNSVSSGMKGGYLAACGVFIGDAVLMFLAWAGVATL----IKTT 72
                                             SEQUENCE FROM N.A.
SETALTAL AG1655;
STRAINE-97426617; PubMed-9278803;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Olunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                   Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342E0DF348C9AD9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%; Score 190; DB 1; 28.2%; Pred. No. 1.4e-08; iive 36; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000274; AAC74868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90823; BAA15593.1; -.
EMBL; D90824; BAA15602.1; -.
ECGENE; EG13505; yeas.
InterPro; IPR001123; -.
Pfam; PF01810; LysE; 1.
Hypothetical protein; Transmem!
TRANSMEM 12 32 PP
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173
208
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                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
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Local St.
57;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII-VETLAWFTVVASLFA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 SFWGGSLSNIENPKTVLVYVTIMPOFINENGNINQQLIILASILTELLAVEWFLFEVVIID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LLAYIPIAAMMVII---PGADTMLVMKNTLRYGPKAGRYNILGLATGLSFWTVIAILGLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IMLFLIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 180.5; DB 1; Length 210; llarity 24.5%; Pred. No. 7.7e-08; Conservative 41; Mismatches 101; Indels 15;
                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 23,4 KDA PROTEIN IN AAPA-SIGV INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                     Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
2A37D9419FDB0A58 CRC64;
                                                                                                                                                                 Bacillus subtilis.
Bacteria, Firmicutes; Bacillus/Clostridium group;
210 AA.
                                                                                                                                                                                             Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 299117; CAB14652.1; -.
EMBL; U93874; AAB80973.1; -.
Subtilist; BG12304; yrhp.
InterPro; IPR001123; -.
Pfam; PF01810; LySE; 1.
Hypothetical protein; Transment
TRANSMEM 50 70 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-141 FROM N.A. STRAIN=168;
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 J
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Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HLII--EKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGR-SFLK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GLLTNLANPKAIIYFGSVFSLFVGDNVGT---TARWGIFALIIVETLAWFTVVASLFALP 174
                                                                                                                                                                                                                                                                    MEDLINE=2043737; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagie W.O., Kowallk D.J., Lagrow M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smith K.a., Spencer D.H., Wong G.K.P., S. Was A., Larbig K., Lim R.M., Smith K.a., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen."

Nature 406:959-964(2000)

-! SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PAO1; White C.B., Young M.D., Hobbs M., Mattick J.S.; WhiteChurch C.B., Young M.D., Hobbs M., Mattick J.S.; Pseudomonas aeruginosa chemotactic transduction genes pill, chpB chpB and downstream genes chpC, chpD and chpE."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%; Score 159; DB 1; Length 203; 27.7%; Pred. No. 3.8e-06; Live 38; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195553C048AAD099 CRC64;
                                                  (Rel. 38, Last sequence update) (Rel. 40, Last annotation update) TRANSDUCTION PROTEIN CHPE.
               203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
               PRT;
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66 PO
89 PO
143 PO
169 PO
21290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U79580; AAC23935.1; -.
EMBL, ABC04479; AAG03806.1; -.
InterPro; IPR001123; -.
Ffam: PF01810; LYSE; 1.
                                     (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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69
123
149
203 AA;
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                            Pseudomonas.
NCBI_TaxID=287;
                                                                                      CHPE OR PA0417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
                                     15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
              PSEAE
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Best Local Si
Matches 59,
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TRANSMEM
SEQUENCE
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CHPE_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | (1) | REDLINE=97061201; PubMed=8905231; RA MEDLINE=97061201; PubMed=8905231; RA MADAJIAN N. HIROSAWA M., Sugiura M., Sasamuco S., Kimura T., Matajian N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Matajian N., Hirosawa M., Tabata S., Shimpo S., Takeuchi C., Wada T., Watanabe A., RA Wanada M., Tasuda M., Tabata S., Ra Vanada M., Tasuda M., Tabata S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Ra Vanada M., Tasuda M., Tabata S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; RT. DNA Res. 3:109-136(1996).

C. 1- SUBCELLULAR LOCATION: INTEGRAL MEMERANE PROTEIN (POTENTIAL).

C. 1- SIMILARITY: BELONGS TO THE RHT FAMILY.

C. 1- SIMILARITY: BELONGS TO THE RHT FAMILY.

C. 1- SIMILARITY: BELONGS TO THE RT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 15.1%; Score 159; DB 1; Length 206; Similarity 26.6%; Pred. No. 3.9e-06; Conservative 39; Mismatches 96; Indels 56; Conservative 39; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
EF493754B8F264AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TAXID=1148;
                                                                                                                                                                                                                       206 AA
                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation updat-
HYPOTHEFICAL 22.0 KDA PROFEIN SLR1627.
175 QMRRG----YQRLAKWIDGFAGALFAGFGIHLI 203
                                                              171 WLRRNTSLFWHRVS-----YAGCGVLLL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- ORLAKWIDGFAGALFAGFGIHLIIS
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 Pr
22041 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D90914; BAA18437.1; -.
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001123; -. Pfam; PF01810; LysE; 1. Hypothetical protein; Transmem 9 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 1
206 AA;
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P74343;
01-x
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Best Local S:
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
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                                                        125 SIVFLAALFPQFIMPQQPQLMQYIVLGVT-----TIVVDIIVMIGYATLAQRIALWI 176
71 AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHL-----FQRAVFVNLTNPK 124
                             AIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWI 187
                                                                                                                                                                                                                                                                                                                                                                                                 Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K., Williams P., Macintyre S., Stewart G.S.A.B.;
submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-i- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                    15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-UTL-1998 (Rel. 36, Last anotation update)
HYPOTHETICAL 21.5 KDA PROTEIN IN ASAR-CDPD INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                              Proteobactería; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                          206 AA.
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POTENTIAL.
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                                                                                         DG------FAGALFAGFGIHLIISR 206
                                                                                                        EMBL; U65741; AAB70019.1; ALT_INIT.
InterPro; IPR001123; -.
Pfau; PF01810; LysE;
Hypothetical protein; Transmembrane
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PO
57 PO
85 PO
136 PO
168 PO
205 PO
21505 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 26.0% 52; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                               Aeromonas salmonicida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
116
148
185
206 AA;
                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
STRAIN=NCIMB 1102;
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=645;
                                                                                                                                                                                        YGGA_AERSA
P70775:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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Matches
                                                                                         188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 LHTLIMVGGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK 127
                                                                                                                                                                                        SEQUENCE FROM N.A.

STARAIN-RIZ / MG1655;
MEDLINE-92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Manlysis of the Bscherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LTSIILSLSPGSGAINTMTTSLNHGYRGAVASIAGLQTGLAIHIVLVGVGLGTLFSRSVI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 MVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE RIT FAMILIA.
-!- CAUTION: THIS IS A CONCEPUAL TRANSLATIO.
BE INTRODUCED IN POSITIONS 60 TO EXTEND THIS ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                               "The novel transmembrane Escherichia coli proteins involved in the amino acid efflux.";
FEBS Lett. 452:228-23(1999).
-i- FUNCTION: CONDUCTS THE EFFLUX OF HOMOSERINE AND HOMOSERINE
                                                                                                    Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                     CHÄRACTERIZATION.
MEDLINE-99313167; Pubmed-10386596;
Zakataeva N.P., Aleshin V.V., Tokmakova I.L., Troshin P.V.,
Livshits V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1164F17738509C8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 144.5; DB 1;
Similarity 20.7%; Pred. No. 5.5e-05;
13; Conservative 44; Mismatches 96;
                                            01-AUG-1992 (Rel. 23, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HOMOSERINE/HOMOSERINE LACTONE EFFLUX PROTEIN.
                  206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
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EMBL; AE000458; AAC76827.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                          Unpublished observations (JUN-1999).
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Transmembrane.
TRANSMEM 5 25
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S30714; S30714.
EcoGene; EG11469; rhtB.
InterPro; IPR001123; -.
Pfam; PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                              CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
148
182
206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Sim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACTONE
                  RHTB_ECOLI
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TRANSMEM
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11;
                                                                                                                                                                           PKAIIYFGSVFSL-FVGDNVGTTARWGIFALIIVETLAWFTVVA--SLFALPQMRRGYQR 182
                                                                                                                                                                                                                                      MAWLHTLIMVGGGLYLCWMGYQMLRGALKKE-AVSAPAPQVELAKSGRSFLKGLLTNLAN 125
                                                                       Gaps
                                                                                                  14 VALMSP-GPDFFFVSQTAVSRSRKEAMMGVLGITC----GVMVWAGIALLGLHLI-IEK 66
                                                                                                                     25;
                                          DB 1; Length 206;
                                                                       91; Indels
DIC2C492CDA0179A CRC64;
                                          10.6%; Score 111.5; DB 26.0%; Pred. No. 0.023; Ive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 VDLLSNAAPIVLDIMKW-----GGIAYLLWFAVMAAKDAMTNK---VEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 LHL-----IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQV----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TVPDDTPLGGSAVATDTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGG 169
                                                                                                                            135 VFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIA-LLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 ------ELAKSGRS-----AIIYFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 105; DB 1; Length 236; Ilarity 20.4%; Pred. No. 0.085; Conservative 36; Mismatches 99; Indels
                                                              Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL,
POTENTIAL,
POTENTIAL.
EE86E8CF037C4727 CRC64;
                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
LYSINE EXPORTER PROTEIN.
 236 AA
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        ΨW.
                                                                                                                                                                                                                                                                                                          EMBL; X96471; CAA65324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    200
236
25425 1
                                                                                                                                                                                                                                                                                                                   InterPro; IPR001123; -. Pfam; PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTALAIKLML 234
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=1718;
                 15-JUL-1998
LYSE_CORGL
P94633;
                                                                                                                                                                                                                                                                                                                                         Transport;
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SEQUENCE
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 PKAIIYFGSVFSL-FVGDNVGTTARWGIFALIIVETLAWF-----TVVASLFALPQMRR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K., Chhabra S.R., Walliams P., Macintyre S., Stewart G.S.A.B.; Guorum sensing in Aeromonas hydrophila and Aeromonas salmonicida: identification of the LuxRI homologs AhyRI and AsaRI and their cognate Nacythomoserine lactone signal molecules."; J. Bacteriol. 179:521-5281(1997).

-: SUBCELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).

-: SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LAMIIPIGAQNAFVLSRGIHRNH-HLLTATLCCLCDLVLIGIGVFGGANLLAASPIGLAL
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                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-1996 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 39, Last annotation update)
10-0MX-2000 (Rel. 34, Last annotation update)
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POTENTIAL.
172DB104473B0B09 CRC64;
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; Pred. No. 0.089;
29; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYORL ----- 203
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                                                                             225 AA
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InterPro; IPRO01123; -1.Pfan; PF01810; LysE; Lyer
Pfan; PF01810; LysE; Lyer
Hypothetical protein; Transmembrane.
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                                                                                  PRT;
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MEDLINE-97431471; PubMed-9286976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 PO
57 PO
85 PO
136 PO
170 PO
24482 MW;
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116
150
225 AA;
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=644;
                                                                             YGGA_AERHY
P52047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
RESULT 12
YGGA_AERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
YGGA_ECOLI
ID YGGA_E
AC P11667
DT 01-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 IMOSPWILLALVTWGGVAFILWYGFGAFKTAMSSNIELASA---EVMKQGR--WKIIATML 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 A----NPKAIIYFGSVFSLFVGDNVGTTARWGIFAL-IIVETLAWFTVVASLFA--LPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alefounder P.R., Bandwin S.A., Perham S.A., Short N.J.;
Alefounder P.R., Bandwin S.A., Perham S.A., Short N.J.;
Identification, molecular cloning and sequence analysis of a gene
cluster encoding the class II fructose 1.6-bisphosphate aldolase, 3
phosphoty depends and a putative second glyceraldehyde 3-
phosphate dehydrogenase of Escherichia coli.",
Mol. Microbiol. 3:723-732(1989).
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                            5
                                                                                                         Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 23.2 KDA PROTEIN IN SBM-FBA INTERGENIC REGION (ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2DAFE27B6A9BE822 CRC64;
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POTENTIAL.
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MEDLINE=89313302; PubMed=2546007;
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EMBL; AAC000375; AAC75960.1; -.
EMBL; X14436; CAA32607.1; -.
PIR; S04736; QQEC5A.
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InterPro; IPR001123; -.
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Pfam; PF01810; LysE; 1.
Hypothetical protein; TTRANSMEM
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                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                             Bacteria; Pr
Escherichia
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Best Local S.
Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jake H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H., Kashimoto K., Inada T., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yamo M.; Submitted (JaN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-37426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Yides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rudd K.E.;
Unpublished observations (AUG-1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                          Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                in
                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-2094 (Rel. 30, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 21.2 KDA PROTEIN IN SRMB-UNG INTERGENIC REGION.
                                                                                                                                                                                                                                                                          Non-ribosomal proteins affecting the assembly of ribosomes transfering coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nashimoto H., Saito N.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                             (In) Nierhaus K.H. (eds.);
The translational apparatus, pp.185-195, Plenum Press,
                                 195 AA.
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EMBL; D60404; -; NOT_ANNOTATED_CDS.
EMBL; AE000344; -ANOTATED_CDS.
EMBL; D90886; BAA16464.1; -.
ECOGENE: EG12445; yfik.
Hypothetical protein; Transmembrane.
TRANSMEM 8 28 POTENTIAL.
                                 PRT;
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                  York (1993).
                                                                                                                                                                                                       NCBI_TaxID=562;
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                                                                                                                                                                          Bacteria; Pri
Escherichia.
                               YFIK_ECOLI P38101;
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RESULT 14
YFIK_ECOLI
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Search completed: May
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XX MEDLINE-98295987;
PURPLINE-98295987;
PURPLINE-98295987;
PURPLINE-98295987;
PURPLINE-98295987;
PURPLINE-98295987;
PURPLINE-98295987;
PURPLINE-PROSEN R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Egglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Envam D., Chillingworth T., Connor R.,
Padcock K., Basham D., Peltwall T., Gentles S., Hamin N., Holroyd S.,
RA Davies R., Deviln K., Feltwall T., Gentles S., Hamin N., Holroyd S.,
RA Diver S., Seeger K., Skelton S., Squares S., Marriyn L.,
RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RR Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
RR Tolor K., Whitehead S., Barrell B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the
RT Complete genome sequence...
RR Rature 393:537-544 (1998...)
R. Mature 393:537-544 (1998...)
CC -I- SIMILARITY: BELONGS TO THE LYSEXYGGA FAMILY.
                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 62 ---FSLAVIDPAAVH-LLSWAGAAYIVWLAWKIATSPTKEDGLQA------KPISFW 108
                                                                                                                                                                                                                                                                                  57 LLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                     Gaps
                                                                                                                                                                                                     1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG----VMVWAGIA 56
                                                                                                                                                                                                                               Mycobacterium tuberculosis.

Batceria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriacee; Mycobacterium.

NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                 117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                             109 ASFALQEVNVKIILY------GVTA-LSTFVLPQTQALSWVVGVSVLLAM 151
                                                                                                                      Query Match 9.6%; Score 101; DB 1; Length 195; Best Local Similarity 22.0%; Pred. No. 0.15; Matches 39; Conservative 32; Mismatches 72; Indels 34;
  POTENTIAL.
POTENTIAL.
POTENTIAL.
5F86B828DDDEC090 CRC64;
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E198975DF088E6E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 20.9 KDA PROTEIN RV0488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 201 AA
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InterPro; IPR001123; --
Fam, PF01810; LysE; --
Hypothetical protein; Transmembrane.
TRANSMEM 25 45 POTENTIAL
TRANSMEM 104 124 POTENTIAL
TRANSMEM 13 153 POTENTIAL
TRANSMEM 169 189 POTENTIAL
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71 91 PO
142 162 PO
195 AA; 21248 MW;
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PRELIMINARY;
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Q9L6N7
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09xf8si bacillus ha
09rif0 yersinia en
0916h7 brucella me
09kf9b bacillus ha
09kr3c bacillus an
09kr75 bacillus an
09rx2 deinococcus
09kx40 vibrio chol
09kx40 vibrio chol
09kx40 vibrio chol
09pg2c0 xylella fas
09km3 vibrio chol
09feff salmonella
09r6ff salmonella
09r6ff salmonella
09r6ff vibrio chol
09kr7 vibrio chol
09km3 vibrio chol
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             1 MLMLFLTVAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                374700
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                           374700 seqs, 117207915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    protein search, using sw model
                                                                                                                                          0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0916N7
09KVF5
09KVF5
09KF81
09L6H7
09KFP9
09KFP9
09KF77
09KSX2
09KSX2
09KSX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9L6N6
Q9R6J5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KVK7
Q9KQQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29R6F8
                                                                                                                                                                                                                                                                                                                                                                                sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                          sp_archea:*
sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                          Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                           sp_mammal:*
sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                           US-09-466-935-4
                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                    SPTREMBL_15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of
                                                                                                                                                                                                  sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          983
313.5
269.5
269.5
221.5
221.5
190
190
174.5
172
167.5
163.5
1153.5
1153.5
1147.5
1147.5
                                                                                                     Perfect score:
                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                    ı
                                                                                                                                                                                                 Minimum DB
Maximum DB
                                    OM protein
                                                                                                                                                                                                                                                                   Database :
                                                                                                              Sednence:
                                                                                                                                                             Searched:
                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
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| 09xbr8 zymomonas m 027538 methanobact 09x4k6 streptcomyce 09v985 drosophila 09wy15 thermotoga 08wy15 thermotoga 08wy15 thermotoga 08wy15 thermotoga 08my19 joinitca ni 09m104 naupactus v 09my19 joinitca ni 09m104 naupactus v 09my104 naupactus v 09my106 streptcomyce 033423 protopterus 09yu10 streptcomyce 059044 shewanalla 0599116 streptcomyce 059040 vibrio chol 006730 bacillus su 006730 bacillus su 006730 bacillus su 006730 ralstonia s | OSKNES bacillus ha<br>OSK707 bacillus ha<br>OSV655 drosophila<br>OSS371 bacillus sp<br>OSKaw6 bacillus ha<br>QSK599 vibrio chol<br>P96675 bacillus su |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|
| Q9XBR8<br>Q27538<br>Q94K4K6<br>Q99K4K6<br>Q99VQ85<br>Q99W15<br>Q99W193<br>Q99K194<br>Q95K36<br>Q95121<br>Q95121<br>Q953934<br>Q953934<br>Q953934<br>Q953936<br>Q953936<br>Q953936<br>Q953936                                                                                                                                                                                                                                                          | Q9KBZ9<br>Q9KBZ9<br>Q9V6J5<br>Q8Z971<br>Q9KAW6<br>Q9KS99                                                                                              |
| 800000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                               | 0000000                                                                                                                                               |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                | 409<br>516<br>697<br>209<br>395                                                                                                                       |
| 111111<br>21100000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                            | <i>.</i> .                                                                                                                                            |
| 1123.<br>123.<br>1115.<br>1106.<br>106.<br>106.<br>106.<br>106.<br>106.<br>106.<br>10                                                                                                                                                                                                                                                                                                                                                                 | 88<br>87.5<br>87.5<br>87<br>87<br>87<br>87                                                                                                            |
| 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                | 3<br>4<br>4<br>4<br>5<br>4<br>7                                                                                                                       |

## ALIGNMENTS

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TNLANPKAIIYFGSVFSLEVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQWRRGY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL 60
                                                                                                                                          Salmonella typhimurium LT2.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
NCBL_TaxID=99287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=SGSC1412;
Waterston R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AFC33323.4; ARF33433.1; -.
SEQUENCE 206 AA; 22498 MW; 080477853FC2733F CRC64;
                                                                                                                                                                                                                                                                                                                                         "The Salmonella typhimurium Genome Sequencing Project.", Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%; Score 983; DB 2; Le 90.8%; Pred. No. 6.8e-74; ive 11; Mismatches 8;
206 AA
                                               Created)
PRT;
                                       01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.8%
Matches 187; Conservative
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g ŏ g Q9KVF5 Q9KVF5;

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LIAEGGALFSAIKIGGGLYLVWYAYNWVRHRQELHMGMGAV---ATSSITPWYVF----- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 IIEKMAWLHTLIMVGGGLYLCWMGYQMLR------GALKKEAVSAPAPQVELAKSGR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: ||: : :: ::|| : | ||::| : :||: | :: ||: | :: ||: | :: ||: || :: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEKMAWLHTLIMVGGLYLCWMGYQMLRGA--LKKEAVSAPAPQVELAKSGRS----FLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia enterocolitica (type 0:8).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; APO01517; BAB06651.1; -.
SEQUENCE 210 AA; 23712 MW; C49C7DE7C86F6F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0C18DA690C479702 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%; Score 269.5; DB 2; ilarity 28.1%; Pred. No. 5.3e-15; Conservative 52; Mismatches 80;
                                                                                                                                                                                                                                                                                                                           27.7%; Score 292; DB 2;
32.4%; Pred. No. 7.3e-17;
Live 37; Mismatches 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POMRRGYORLAKWIDGFAGALFAGFGIHLI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1995) to the
EMBL: 247200; CAB61500.1;
INTERPO: PPRO1123; -.
PFAM: PFF01810; LYSE: 1.
SEQUENCE 212 AA; 22790 1
                                                                                                                                                                                                                                                                                                                                    Query Match 27.7%
Best Local Similarity 32.4%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
Versinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=34054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIREL TOR NIG661 / SEROTYPE 01;
MEDIZER=1 TOR NIG661 / DEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 YLVKQQPMLFNLLQLAGGSYLLYLGAGALQSVWAQKNASTPTHSPAPSI-LGNRRQAFTK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TNLSNPKAIIYFGSVFSLFVGDNVGAAARWGIFALITLETLAWFTVVASLFALPKMRRGY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVS----APAPQVELAKSGRSFLK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 AA; 23485 MW; B5B83AC3804E5E71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VC0191.
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                            222 AA
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99K851;

01-CCT-2000 (TrEMBLrel. 15, C

01-CCT-2000 (TrEMBLrel. 15, I

01-CCT-2000 (TrEMBLrel. 15, I

BH2932 PROTEIN.
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EMBL: AE004109; AAF93367.1;
IIGR: VC0191; -
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Query Match Best Local S

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Q9RMX0;
01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ARAVLIDRLSGLVLIALAIRVL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004412; AAF96744.1; -.
TIGR; VCA0846; -.
SEQUENCE 204 AA; 21719 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCA0846.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=666;
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Matches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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Q9KLA0
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                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=16M;
STRAIN=16M;
STRAIN=16M;
STRAIN=16M;
STRAIN=16M;
STRAIN=16M;
Clonding, nuclectide sequence, and expression of the Brucella melitensis sucB gene coding for a dihydrolipoamide succinyltransferase homologous protein.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF235020; AAF43702.1; -.
SEQUENCE 212 AA; 23158 MW; OC21287CEA665F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTLIMVGGGLYLCWMGYQMLR-GALKKEAVSAPAPQVELAKSGRSFLK----GLLTNLAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 PKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBL_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 251.5; DB 2; Length 212; 29.9%; Pred. No. 1.6e-13; tive 41; Mismatches 88; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch
1 Similarity 28.3%; Pred. No. 2.3e-09;
63; Conservative 39; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001508; BAB04148.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508; BAB04148.1; -. 20317 MW; 9FED148C8E8DD3F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA
                                                                   212 AA
                                                                                                                                    Created)
                                                                   PRT;
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                                                                                           Q9L6H7;
01-CCT-2000 (TIEMBLIEL 15, Crea 01-CCT-2000 (TIEMBLIEL 15, Las) 01-CCT-2000 (TIEMBLIEL 15, Las) AMNO ACID EFFLUX-LIKE PROTEIN. Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, BH0429 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 WIDRTSGVVFIALGLKL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 WIDGFAGALFAGFGIHL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local ;
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Matches 5
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STRAIN=EL TORN NIG961 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 LLTNLANPKAIIYFGSVFSLFVGDNVGTTARWG-----IFALIIVETLAWFT---- 165
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|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| 
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                                                                                                                                                                                                                                                                                                                                                            63 ALIYQSALAFTVVKYAGAAYLLYLAWKAFQE-----KGEGLSID-KQTTLA-YGALYKKG
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0846.
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171 SGTFRDRLLKNSRFNEYMNIAATIIFIGLGLKLMTTQ 207
                                                                                  181 ------QRLAKWIDGFAGALFAGFGIHLIISR 206
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                                                                                                                                                                     PRT;
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01-OCT-2000 (TrEMBLrel. 15,
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Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                       LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                       122 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII--VETLAWFTVVASLFALPOMRRG 179
                                                                                                                                                                                                                                                                                                                                                                                                                              119 DMLNPKATLFYLAIFTQVIEPNTNIFVQ-SVYGLTVWSVEIL-WHMVLVFFLTHKSVRNY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 MLFLIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Gaps
                                                                                                                                                                                                                                                                                                        2 IMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

OKINARA R.T., Cloud K., Hampton O., Hill K.K., Keim P., Lamke G.,

Kumano S., Manter D., Martinez Y., Svensson R., Tatum L.R.,

Brown A.E., Jackson P.J.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF188935; AAF13668.1;

INTERPRO; IPR001123;

PPAM; PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 186; DB 2; Length 208;
25.3%; Pred. No. 4e-08;
.ive 49; Mismatches 83; Indels
                                                                                                                                                                                                                                                         Length 205;
                                                                                                                                                                                                                                                      18.0%; Score 190; DB 2; Length 20
26.1%; Pred. No. 1.9e-08;
tive 50; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP001519; BAB07214.1;
SEQUENCE 208 AA; 23158 WW; CAD7A46D63B8E45A CRC64;
                                                                                                                                                                                                                     205 AA; 22900 MW; 6DC91EE968B524B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9K775 PRELIMINARY; PRT; 208 AA.
Q9K775;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus halodurans.
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 55; Conserv
                                    Bacillus anthracis.
                                                                                                                                                                                                        Plasmid.
SEQUENCE
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                                    121 VLNPKVAIFYLFFFPPPVNYQSANISLQLCILGLIFIIMTA---IIFSIF------GYF 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 EKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVS-----APAPQVELAKSGRSFL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE:
MEDLINE=20036896; PubWed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Elsen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 FLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLII 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome Sequence of the Radioresistant Bacterium Deinococcus radiodurans R1.";
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Science 286:1571-1577(1999).
EMBL, AB002037; AAF11548.1; -.
INTERPRO; IPR000719; -.
INTERPRO; IPR001123; -.
PROSTIE; PRO1810; LySE; 1.
SEQUENCE 241 AA; 25161 MW; A4017ABFEDB60374 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 174.5; DB 2; ilarity 29.1%; Pred. No. 4.2e-07; Conservative 37; Mismatches 80;
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EMBL; AE004427; AAF96896.1; -.
TIGR; VCA1000; -.
SEQUENCE 209 AA; 22451 MW; F433B755AFCA4243 CRC64;
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                                                                                                                                                                    Conservative
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                                                                                                                                              Local Similarity
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01-0CT-2000
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                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed=10952301;

Heldelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=EL TORN N16961 / SEROTYPE 01;
STRAIN=EL TORN N16961 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonnald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 IMVGGGLYLCWMGYQMLRGALKK----EAVSAPAPQVELAKSGRSFLKGLLTNLANPKAI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 IYFGSVFSLFVGDNYGTTARWGIFALI-IVETLAWFTVVASLFALPQMRRGYQRLAKWID 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | || :| :| || :| || 75 VKMVGAAYLIWLGISSLRSLMKTGQGIEVASLAHAQFRLT---RSLREGFLSNVLNPKTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 VFYLAFLPQFINPDYSPLAQSLLMALIHFAIAMVWQCGLAGALSSAKNLLKNASFMRWME 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AA; 22832 MW; 1DBDCBA37566C394 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) HYPOTHETICAL PROTEIN VC1421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%; Score 172; DB 2;
23.7%; Pred. No. 5.9e-07;
tive 38; Mismatches 105
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01-OCT-2000 (TrEMBLrel. 15, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last ann
HYPOTHETICAL PROTEIN VCA1000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004221; AAF94578.1; -. TIGR; VC1421; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 GTTGVVLVALGIKLLLEK 209
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                                                                                                                                      NCBI_TaxID=666;
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REDILINGALOSON, T. FUDMOGRIGHOUSE, Baid G.S., Baptista C.S.,
RA BINDSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Abrete F.A., Bringson A.J.G., Reinach F.C., Arruda D.E., Baid G.S., Baptista C.S.,
RA Buerco W.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bringson R.R.S.,
RA Buerco M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Buenco M.R.P., Canargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto D.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnicari M.P., Ferreira M.S., Gomes S.L., Gruber A.,
RA Garnicari M. Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnicari M. Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnicar M., Goldman G.H., Goldman M.H.S., Machado J.A.,
RA Marques M.V., Madeira A.M.B.N., Madeira H.M.F., Marlunc C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.A., Marsukuma A.Y.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Gensa V.E., Jr., de Silva A.M., de Silva M.A., Jr., Martins E.M.,
RA Gensa V.E., Jr., de Silva M.M., de Silva M.A., Tsuhako M.H.,
RA Gensa V.E., Jr., de Silva A.M., de Souza A.J.M.,
RA Gensa M.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.
REMBI, ABON04079; Arres5511; -.
                                                                                                                                                                                                                                                                                                                                     59 GLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                61 GVSALIAMNPLALNVLHLLGGAYLLKMAWDCLRA----DAAQAPTLDEAQAVAKTFYQRA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                    3 MLFLTVAMVHIVA----LMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALL 58
                                                                                                                                                                                                                     119 LLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL----
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    Length 209;
                                                                                    Indels
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Last sequence update)
Last annotation update)
    5;
15.9%; Score 167.5; DB 2 26.0%; Pred. No. 1.4e-06; Live 37; Mismatches 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINE D. TOR NIG961 / SEROTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Ralzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                            122 NIANPKAIIYFGSVFSLFVGDNVGTTAR---W-GIFALIIVE--TLAWFTVVASLFALPQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWRGGSTLKVSESVESDKN--VFVQGVIV 120
                                                                                                                                                                                                                    62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                           122 NLANPKAIIYFGSVFSLFV--GDNVGTTARWGIF------ALI-----IVETL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LILFIVAC----LAINMIPGPDVIYIVSNTMKGKLVTGFKAAMGLGVGVFVHTLAASLGLS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Gaps
                                                                                                          28; Gaps
                                                                                                                                                                   LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                             2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 208;
                                                                    Length 213;
                                                                  ; Score 163; DB 2; Length 21; Pred. No. 3.3e-06; 35; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
PFAM, PF01810; LYSE; 1.
SEQUENCE 213 AA; 23614 MW, E97242DD507C8065 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 14.8%; Score 155.5; DB 2; Best Local Similarity 23.8%; Pred. No. 1.3e-05; Matches 50; Conservative 43; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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EMBL; AE004372; AAF96263.1; -.
TIGR; VCA0355; -.
                                                                      15.5%;
                                                                    Query Match
Best Local Similarity 25.39
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   191 TWFNYV 196
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                 SEQUENCE
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77 GGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGS 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LSPGSGAINTMTTSINHGYRGAVASIAGLQTGLGIHIVLVGVGLGTLFSRSLLAFEILKW 77
                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella. NCBI_TaxID=99287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                           "The Salmonella typhimurium Genome Sequencing Project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
14.6%; Score 153.5; DB 2;
Best Local Similarity 23.4%; Pred. No. 1.9e-05;
Matches 47; Conservative 38; Mismatches 91;
                                                                                                                206 AA.
S----QRYSRGLEGVSGVLLIGLASKVAIS 206
                                                                                                                                                        Created)
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                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ALNKAFGSLFMLVGALLASAR 204
                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                    Salmonella typhimurium LT2.
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-SGSC1412;
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ne: 247 sec
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Q9L6N6;
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us-09-466-935-4.rst

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seq_documentation_block:
LOCUS A2576789 407 bp DNA GSS 08-DEC-2000
DEFINITION 01al2 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
ACCESSION A2576789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="01a12"
/clone_lib="Shot-gun genomic library of Rhizobium strain
ANU365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: M13; derivative strain of NGR234 cured of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viprey, V., Rosenthál, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome GenomeBiology.com 1 (6), 0014.1-0014.7 (2000) Contact: Virginie Viprey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACACGCTCTATGCCGCGCTCGGCGTCACGTCTTGCATCTGGTGCC 208
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Gaps: 2
Percent Identity: 30.000
          834
1075
1578
561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
          39.56
56.33
96.10
26.03
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/db_xref="taxon:394"
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      147.60
144.84
140.68
150.86
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a 126 c
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Ratio: 1.797
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                                                                                                                                                          seq_name: gb_gss23:AZ576789
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      gb_est82:BF027022
gb_est89:BF581425
gb_est92:BF782441
gb_est12:AA817286
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COMMENT
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AUTHORS
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Library normalized by Jihwan Song
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: Kanopus clone distribution information for
this library can be found through Research Genetics, visit their
below when ordering this clone: Source lab clone id - xlnnga005b04
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dg18a02.y1 Xenopus laevis gastrula non normalized Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnnga005b04 5' similar to TR:Q9RSXZ ONSERVED HYPOTHETICAL PROFEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sandy Ciffton, Ph.D.
Contact: Sandy Ciffton, 19.D.
Wash Wash Waropus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                      85 etGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAla 101
                                                                             102 ProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGl 118
                                                                                                                                                                                                                                                        107 GGGGGAGGCTCTCGCGCTGGGCG.....AGCTTTCGACAGGG 70
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                                                                                                                                                                                                                                                                                                                                 118 yLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyr 131
                                                                                                                                                                                                                                                                                                                                                                            69 GGGGCTGAGGCCTGATGAANCCGAAGGCCTATCNCTTC 30
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Location/Qualifiers
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BF614897.1 GI:11787968
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314 286 1810
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LOCUS BF614897
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KEYWORDS
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SOURCE

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(pases 1 to 443)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG038404 443 bp mRNA EST 24-JAN-2001 493404 443 bp mRNA gastrula non normalized Xenopus laevis cDNA clone XENOPUS_SOURCE ID:XIDNG#2009p16 5' similar to TR:09RSXZ 09RSXZ CONSERVED HYPOTHETICAL PROTEIN. ;, mRNA sequence.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 GCCCGCGTCATCGGTGAGCGATCCTCATCAATCTGCTGAACCCGAAACT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 GTCGATCTTTTTTTTTTCTGCCGCAGTTCATCGCGCCGGATGAGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyargSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 TCGGCATCGTGCCGCATCTGCTCGCCGCCATCACCGGTCTTGCCGCCATC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 AGATCGATGAAACGAGGCAGCCG......CAAAAAGCC 284
                                                                                                                                                                                                                                                                                                                                                                                                                           14 ValAlaLeuMetSerProGlyProAspPhePheValSerGlnThrAl 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLe 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 uTyrLeuCysTrpMetGlyTyrGlnMetLeuArg.....GlyAlaLeuL 95
1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 CTGCACACCAGTGCGCTGGCCTTTAGCGTGGTCAAATATCTGGGGGTCGC
                                                                                                                                                                                                             Percent Identity: 26.897
                                                                                                                                                  Length:
                                                                                                                                                                                      Gaps:
96
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                                                                                                                                                                                                                                                                                                                                                                   to: 428
   9
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   127
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1. .535
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10w stringency conditions."
34 a 176 c 133 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-SN0012-010
400-001-q02x=23000-04-01x*t=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence steps: 533.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

      seq_documentation_block:
      22-MAY-2000

      LOCUS
      AWB63870
      535 bp
      mRNA
      EST
      22-MAY-2000

      DEFINITION
      PW4-SN0012-010400-001-902 SN0012 Homo sapiens CDNA, mRNA sequence.

      ACCESSION
      AWB63870

      VERSION
      AWB63870.1 GI:7997920

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shofgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                            112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                                                                314 GCCCGCGTCATCGGTGAGGCGATCCTCATCAATCTGCTGAACCCGAAACT 363
                                           95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111
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Gaps: 1
Percent Identity: 39.683
                                                                                                                                                                                                                                                                                                                                                  364 GTCGATCTTCTTTTTGCCTTCCTGCCGCAGTTCATC 400
                                                                                                                                                                                                                                                                                                              128 allelleTyrPheGlySerValPheSerLeuPheVal 140
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2.458
76.190
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Ratio:
Percent Similarity:
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COMMENT
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
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/EcoRI-XhoI cut coNA was then ligated into Unizap-XR
/Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end SS-library phagemids were prepared from the same library by
PCR) to Cot-onega of Il. After removal of hybridization
to bicinylated driver (prepared from the same library by
PCR) to Cot-onega of Il. After removal of hybridization
to bicinylated driver (prepared from the same library by
the ss-phagemids were made double stranded and
electroporated into Top-10 F'. Original library
contruction by Brucce Humberg (Cho et al. 1991 Cell 67,
library.
library.
                                                                                                                                                                                                                           Email: set@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xanopus clone distribution information for
clone distribution: Asnopus clone distribution information for
whis library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnnga009pl6
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
Other_ESTs: dg34h08.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
181 314 286 1800
Fax: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||| :::||||:::::::: ||||:::
232 CTATCTGCTCTACATGGCGTGGAACACGCTGCAGGAGAATGGCGCGCTGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 ValAlaLeuMetSerProGlyProAspPhePhePheValSerGlnThrAl 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
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Gaps: 2
Percent Identity: 25.581
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1.595
57.364
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US-09-466-935-4 x BG038404
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          COMMENT
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seq_name: gb_est96:BG116685
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LOCUS BG116685
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TITLE
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-SN0012-030
400-001-q02&t2=2000-04-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 533.
Location/Qualifiers

1. 535
Location/Qualifiers

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(Dases 1 to 535)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
Locus AW863932 535 bp mRNA EST 22-MAY-2000
DEFINITION PM4-SN0012-030400-001-902 SN0012 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW863932
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                  185 GGATTTCGCCGTGGTGGTGCGTGAAGCGTGACCACGGCCGCGCGTGTG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW863932,1 GI:7997982
alignment_block:
US-09-466-935-4 x AW863870/rev
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Fax: +55-11-2707001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1305)

I (bases 1 to 1305)

I (bases 1 to 1305)

INIH-WGC http://wgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

I (brighting 1 to 1305)

I (brighting 1 to 1305)

Email: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLOG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAMI0151 row: h column: 19

High quality sequence stop: 182.

Location/Qualifiers
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/clone=line=Wilh_MGC_88"
/tissue_type="dedenocarcinoma, cell line"
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/tissue_type="dedenocarcinoma, cell line"
/inote="Organ : small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: Salf; Cloned unidirectionally;
oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

a 463 c 347 g 38 t
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602317876F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4417986 :
                                                                                                                                                                                                                                                                                                                                    235 TTTTTGACCGTAGCCTTGATTCACTTGTTGCAGTGGCGAGCCCGGCCC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 oAspPhePhePheValSerGlnThrAlaValSerArgSerArgLysGlu. 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaGl 54
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                                      Gaps: 1
Percent Identity: 39.683
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/db_xref="taxon:9606"
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                                                                                                                                  alignment_block:
US-09-466-935-4 x AW863932/rev
118.00
2.458
76.190
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                                    This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
     Photorhabdus luminescens
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="PLG01899"
/clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size
kb) and then cloned into M13 Janus."
in 164 c 114 g 138 t 4 others
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|179 TGATGAGCGCAACTTTGTGCGGTCAGTGATGGTTTTCTGATTGGTGTC 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 MetValTrpAlaGlyIleAlaLeuLeuGlyLeuHis...LeuIleIleGl
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Gaps: 13
Percent Identity: 25.980
                                                                                                                                                                                                                                                   Contact: ffrench-Constant RH
Contact: ffrench-Constant RH
Department of Balology and Blochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="W14"
/db_xref="taxon:29488"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Forward Class: shotgun.
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US-09-466-935-4 x AQ991044/rev
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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MEDLINE
COMMENT
                                                                                       REFERENCE
AUTHORS
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/note="Vector: pla2917; Genomic DNA from Rhodobacter sphaeroides was prepared and partially digested with Sau3A1. Size selected (20kb) fragments were subcloned into the BglII site of the cosmid vector pLA2917 (Allen, L. N. and R. S. Hanson, 1985, Journal of Bacteriology, 161:955-962. The library was then ordered around
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choudhary, M., Mackenzie, C., Nereng, K., Sodergren, E., Weinstock, G.M. and Kaplan, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736H1C0930305 Rhodobacter sphaeroides 2.4.1 genomic DNA library Rhodobacter sphaeroides genomic clone 736H1C0930305 similar to c (D64002), DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodobacter sphaeroides.
Rhodobacter sphaeroides
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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chromosome II is a true chromosome
Microbiology 143, 3085-3099 (1997)
98015398
                          ........LysAlaIleIleTyrPheGlySerValPheSerLeuPheVal 140
                                                                                                                                                                                                                                                                                                                                                                                             156 elleValGluThrLeuAlaTrpPhe.....ThrValValAlaSerL 170
                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                             ValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPh 115
                                                                                                                                                                                                                                                                                             141 GlyAspAsnValGlyThrThrAlaArg...TrpGlyIlePheAlaLeuIl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 euPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrp 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 GGTTTTCCCCTGTGTTAAGTAAGCCGCTTTCTCAACGGATT..... 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mackenzie, C.
Department of Microbiology and Molecular Genetics
The University of Texas Health Science Center
6431 Fannin St., Houston, TX 77006, USA
Tel: (713) 794-1742
Fax: (713) 794-1782
                                                                                                                                 265 TIGGCGGGTCATIGCGATTATCTTTGCGGTCACTTGGTTAAATCCGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rhodobacter sphaeroides"
/strafh=""2, 4.17"
/db_xref="taxon:1063"
/clone="736H1C0930305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mackenz@utmmg.med.uth.tmc.edu
Seq primer: pBluescript SK (~) T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. coli S17-1"
                                                                                               115 eLeuLysGlyLeuLeuThrAsnLeuAla....
                                                                                                                                                                                                                           215 TTTATTTAGACACCATTGTTGTTCTGGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 IleAspGlyPhe 190
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chromosome II of Rhodobacter sphaeroides (Choudhary et al., 1994, Journal of Bacteriology, 176:7694-7702). The cosmids were then digested with a variety of restriction enzymes (BamHI, EcoRI, BqIII, PStI, ECORV, NoII and DNASEI) and restriction fragments subcloned into the respective multiple cloning site sites of pBluescript SK (-). Note BgIII fragments were subcloned into the pBluescript bamHI site. DNASEI fragments were subcloned into the EcoRV site. All subclones were transformed into E. coll XIIBlue MRF'. All fragments were then sequenced and the sequences where possible were assembled using the GCG program GELASSEMBLE.

25 a 200 c 210 g 166 t 8 others
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LOCUS BE872275 1060 bp mRNA EST 20-OCT-2000
DEFINITION 601446314F1 NIH_MGC_65 Homo sapiens CDNA clone IMAGE:3850491 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 luAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 79
Gaps: 1
Percent Identity: 29.114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeu 82
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: B07708 from: 1 to: 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE872275
BE872275.1 GI:10321051
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1.926
59.494
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US-09-466-935-4 x B07708
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Ratio:
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| Plate: LLAM9569 row: k column: 04<br>High quality sequence stop: 468.                                                                                                                                                                                                                                         |                                                         |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------|
| FEATURES Location/Qualifiers  source 1, .1060  /organism="Homo sapiens"  /db_xref="taxon:9606"                                                                                                                                                                                                                | 136 PheserLe<br>      <br> 324 TICTICT                  |
| /clone=_lib="NIH_MGC_65"<br>/clone_lib="NIH_MGC_65"<br>/tissue_type="adenocarcinoma"<br>/lab_host="DH10B (phage-resistant)"<br>/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;<br>Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.<br>Average insert size 1:8 kb. Library constructed by Life | 141 yAspAsnV. 1:: 274 CATCTCTT 158 alGluThr :::         |
| Technologies."  BASE COUNT 309 a 378 c 283 g 90 t  ORIGIN                                                                                                                                                                                                                                                     | 224 GCCGCAGG<br>162 AlaTrpPh<br>:::   ::                |
| alignment_scores: Quality: 90.50 Length: 279 Ratio: 0.838 Gaps: 13 Percent Similarity: 38.710 Percent Identity: 19.713                                                                                                                                                                                        | 174 AGCTGGCT<br>178 gGlyTyrG<br>159                     |
| 170075 (Text                                                                                                                                                                                                                                                                                                  |                                                         |
| Align seg 1/1 to reverse of: BE872275 from: 1 to: 1060                                                                                                                                                                                                                                                        | seq_documentation<br>LOCUS BE795                        |
| 13 IleValalaLeuMetSerProGlyProAspPhePhePheValSerGlnTh 29 :::    :::                                                                                                                                                                                                                                           | DEFINITION 60159  RRNA ACCESSION BE795 VERSION BE795    |
| 29 ralaValSerArgSerArgLysGlualaMetMetGly                                                                                                                                                                                                                                                                      | ×                                                       |
| 42valLeuGlyIleThrCysGlyVal 49                                                                                                                                                                                                                                                                                 | Mamma<br>REFERENCE 1 (b<br>AUTHORS NIH-M<br>TITLE Natio |
| 50 Metval51<br>                                                                                                                                                                                                                                                                                               |                                                         |
| TrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMet.                                                                                                                                                                                                                                                             | Tissu<br>cdna<br>cdna<br>cdna<br>dna                    |
| 68                                                                                                                                                                                                                                                                                                            | Clon<br>found<br>Plate<br>High                          |
| 73 LeulleMetValGlyGlyGlyGlyLeuTyrLeuCysTrpMe 85 ::::: :::         :::     618 GTCGTGTCTGGGTGGTCCTGCGTGGTGTGTGTGTCTGGAT 569                                                                                                                                                                                    | FEATURES<br>Source                                      |
| 85 tGlyTyrGlnMetL 90<br>                                                                                                                                                                                                                                                                                      |                                                         |
| 90 euArgGlyAlaLeuLysLysGluAlaValSer 100                                                                                                                                                                                                                                                                       |                                                         |
| 101 AlaproAlaProGln                                                                                                                                                                                                                                                                                           |                                                         |
| 106ValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyL 119<br>:::                                                                                                                                                                                                                                                        | BASE COUNT 2<br>ORIGIN                                  |
| 119 euLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerVal 135                                                                                                                                                                                                                                                    | alignment_scores:                                       |

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; BE795531 1183 bp mRNA
ITION 601592515F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946562 5'
                                                                                                                                                                                                                                 136 PheSerLeuPheVal.....Gl 141
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BE795531.1 GI:10216729
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seq_documentation_block:
LOCUS BF972121 1749 bp mRNA EST 22-JAN-2001
DEFINITION 602240161F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328918 5',
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                                                                                                                                                                                                                                     111 CTGATGCTGAGGGGGATGACTTTGAACTTCTGGACCGAGTCGGAGCTGAG 460
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                                                                                                                                                                                                                                                                               32 rArgSerArgLysGluAlaMetMetGlyVal...... 43
                                                                                                                                                                                              16 LeuMetSerProGlyProAspPhePhePheValSerGlnThrAlaValSe 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa
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Percent Identity: 23.744
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90.50
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numen.

NISM Homos appiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;

Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.

(1 bases 1 to 1749)

NE I (bases 1 to 1749)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Inchinal institutes of Health, Mammalian Gene Collection (MGC)

Total: (301) 496-1550

Tissue Procurement: APCC

Conda Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

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CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Ling Hong/Rubin Laboratory

CONDA Library Preparation: Library Constructed > 339.

10.1749

And Library Library Constructed > 500pp for average insert size

Alab.host="Hamber Hong" Priming of California, Berkeley)

Note="Organ: uterus; Vector: pORMs made by oligo-dr priming of Gerald M. Rubin (University of California, Berkeley)

IN RF (Life Technologies). Note: this is a NIH_MGC

Library.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rAlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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1.104 Gaps: 12
47.674 Percent Identity: 24.419
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US-09-466-935-4 x BF972121/rev
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Length:

90.06

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/Clone=lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/tab.host="PHIOB (phage-resistant)"
/note="logan: mascle; Vector: pOTB7; Site_1; ECORI;
Site_2: XhOI; CDNA made by oligo-dT priming.
Site_2: XhOI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhOI sites using the following 5' adaptor: GGCGCAGGG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
43 a 498 c 538 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tel: (301) 496-1550

Tel: (301) 496-1550

Tissue ProberLetrausbergenih.gov

Tissue Procurement: Arrayed

Tissue Procurement: Arrayed

DNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing Dy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: Incyte Genomics, Inc.

Clone distribution: McC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: Licinloge row: f column: 11

High quality sequence stop: 338.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LOCUS BF310123 1866 bp mRNA EST 21-NOV-2000
DEFINITION 601893343F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4138762 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                        134 ServalPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTr 150
                                                                                                                                                                                                                            504 TTGCGTGCAGTGCGGTGAGTGGAGTGG.....GGGCGAGGCGGG...., 466
......TIGGTGTGTTTCGGC 637
                                                                                                                                                                                       150 pGlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValV 167
                                                                                                                                                                                                                                                                                                                   167 alAlaSerLeuPheAlaLeuProGlnMet...ArgArgGlyTyrGlnArg 182
                                                                                                                                                                                                                                                                                                                                                                               554 CTTGCGTCTCGGTGTCTGTTCCGGTGCTTTTCCTTCGGGGTATTCGGACG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                              183 Leu...........AlaLysTrplleAspGlyPheAlaGlyAlaLe 194
                                                                                                                           636 TGTTTGTGGGGGGGGTTGTGACCGCGTTGTGTGTCTCCTGTGGTTTGCTGTG
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/db_xref="taxon:9606"
/clone="IMAGE:4138762"
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alignment\_scores:

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C117C8 687 bp DNA GSS 03-DEC-2000 Ciona intestinalis genomic fragment, clone 17C8, genomic survey
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Simmen,M.W., Leitgeb,S., Charlton,J., Jones,S.J., Harris,B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmer, M.W., Leitgeb, S., Clark, V.H., Jones, S.J. and Bird, A. Gene number in an invertebrate chordate, Ciona intestinalis Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......AlaGlyAl 193
                                                                                                                                                                                                                                                                                                                                                                                     112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 lyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeu 161
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                                                                                                                                                                                                                                                                                                                                  62 LeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl
                                                                                                                                                                                                                                78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL
                                                                                                                to: 1866
                Percent Identity: 21.667
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  Gaps:
                                                                                                                Align seg 1/1 to reverse of: BF310123
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GSS; genome survey sequence.
Ciona intestinalis.
Ciona intestinalis
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ORIGIN
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TITLE
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KEYWORDS
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                                                                             3 (bases 1 to 687)
Simmen,M.W. and Bird,A.
Sequence analysis of transposable elements in the sea squirt, ciona
                                                                                                                                                                                                                      Direct Submission
Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's
Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
VCLARR@srv0.bio.ed.ac.uk
Vector: pBluescript KS.
Location/Qualifiers
                                                                                                                                                                              4 (bases 1 to 687)
Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W.
\mbox{Clark,V.H.} and \mbox{Bird,A.} Nonmethylated transposable elements and methylated genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 TIGGIICAGCGIGICIGAATCACTCTGGICAGIATICTIATCCCGCTCGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|||||||||::::::
153 TTATGGGAGTGATTGCCACACCGTGT......ATTGTTGCCTCCCTG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 GGATCAGTICCCGGCAAIGGCGGGTATGGIGGAAGCITITGCCAIGCTGG 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 ......LeuLysLysGluAlaValSerAlaProAlaProGlnV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 pPhePhePalSerGlnThrAlaValSerArgSerArgLysGluAlaM 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LeuThrValAlaMetValHisIleValAlaLeuMetSerProGlyProAs 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLeu.....
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Gaps: 13
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                                                                                                                                         Mol. Biol. Evol. 17 (11), 1685-1694 (2000)
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                                 chordate genome
Science 283 (5405), 1164-1167 (1999)
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143 c 188 a
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US-09-466-935-4 x CI17C8
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JOURNAL
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                 TITLE
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(Stratagene) and Supersoript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lower suppression whetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases I to 965)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

NL Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert-Strausbergenih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

High quality Sequence stop: 655.

High quality Sequence stop: 655.
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                                                                                                                                                                                                                                                                                                                                                              575
                                                                                                                                                                                                                                                                                                                                                                                                                     161 uAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGlnMetArgA 178
                                                                                                                                                                                                                                                                                                    161
CTGAGACGGATATATCTGGCCGTATTTGTTCCACATTTAAGAAAGGCGAA 469
                                                                                                                                                                               132 heGly.....SerValPheSerLeuPheValGlyAspAsnVal 144
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::: TTTGTATGAACGCTTTCCCGGGCANGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 rgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......GGAGTGGTGTTATG
                                                             119 ...LeuLeuThrAsnLeu.....AlaAsnProLysAlaIleIleTyr.P
                                                                                                                    470 GACCTGAGACAGAACCTTTAATCGAATGGCATACGCTCAATGCTGTATTT
                                                                                                                                                                                                                                                                                                145 GlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLe
                                                                                                                                                                                                                      Location/Qualifiers
1. .965
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BE515205.1 GI:9722420
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Estrausbergenih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov.c column: 15
http://image.lln.gov.c column: 15
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http://image.lln.gov.c column: 15
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Average insert size 1.6 kb. Constructed by Life
Average insert size 1.6 kb. Constructed by Life
a 195 c 201 g 178 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 rPheLeuLysGlyLeuLeuThrAsnLeu......AlaAsnProLysA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 eMetValGlyGlyGlyLeuTyrLeuCysTrpMetGly......
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Gaps: 10
Percent Identity: 28.966
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US-09-466-935-4 x BF584020/rev
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LOCUS BF584020 720 bp mRNA EST 12-DEC-2000
DEFINITION 602096258F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4216262 5',
ACCESSION BF584020
VERSION BF584020.1 GI:11657738
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||:::||||||:::594 ATACATCGGATCTCTGGTGTGTGTGTGG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 PheAlaLeullelleValGluThrLeuAlaTrpPheThrValValAlaSe 169
                                                                                                                                                                                                                                                                                                                                                   844 GGCGGTCTGACTCCGCGCAGCAGCCACCGCGCTTCAAGGGCGGGTTACA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......SerAlaProAlaProGlnValGluLeuAlaLysSer..... 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 CCAAGTGCACCCATTCTCCTAGGGACTCACGGATTCACCACGATTCTTCT 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 lyThrThrAlaArgTrpGly.....Ile 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 GITATITAACAAAAGAGIGGCIAGAAGACICIGGCAGAGAGG..... 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 rpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleHisLeu 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....CAAGGATTTAGACCCCACGTGAGGTCAGGGGTTGGAGATGAAACT 357
                                                                                                                                                                                                                                                                                                               84 TrpMetGlyTyr.....GlnMetLeuArgGlyAlaLeuLysLysGluAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeu.AlaAsn.....
                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: BE515205 from: 1 to: 965
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Gaps: 9
Percent Identity: 24.468
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US-09-466-935-4 x BE515205/rev
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1.099
43.085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 IlelleSerArg 206
                                                                                                                Percent Similarity:
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                                    alignment_scores
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